SEQUENCE LISTING

```
<110> Ballinger, Dennis
      Loeb, Debra
      Montgomery, Julie
      Tang, Y. Tom
Zhou, Ping
      Goodrich, Ryle
      Liu, Chenghua
      Asundi, Vinod
      Zhao, Qing
      Wehrman, Tom
      Drmanac, Radoje
      Ren, Feiyan
      Qian, Xiahong
Wang, Dunrui
<120> MATERIALS AND METHODS RELATING TO LIPID METABOLISM
<130> 28110/35915A
<150> US 60/197,137
<151> 2000-04-14
<150> US 09/714,936
<151> 2000-11-17
<150> US 09/667,298
<151> 2000-09-22
<150> US 09/631,451
<151> 2000-08-03
<150> US 09/598,042
<151> 2000-06-20
<160> 45
<170> PatentIn version 3.0
<210> 1
<211>
       1858
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222>
       (46)..(1143)
<220>
<221> misc_feature
<222> (46)..(1143)
\langle 223 \rangle n = a or c or g or t
<400> 1
cccacgcgtc cgggcctccc tccacctgtc ttctcagagc agata atg gca agc atg
                                                                         57
                                                    Met Ala Ser Met
                                                                        105
get gee gtg etc ace tgg get etg get ett ett tea geg ttt teg gee
Ala Ala Val Leu Thr Trp Ala Leu Ala Leu Leu Ser Ala Phe Ser Ala
                     1.0
                                          15
```

Start Start

113

25 T

D1

							gac Asp							153
							cat His 45							201
							gag Glu							249
_		-	_	_	_		ctg Leu	_		_		_		297
							cgg Arg							345
							ccc Pro							393
							ttg Leu 125							441
							gcc Ala							489
							gac Asp							537
							ctg Leu							585
							gag Glu							633
							cac His 205							681
							ccc Pro							729
					_		ctc Leu	_	_	_	_	_		777
							ctg Leu							825
_	_	-				gaa Glu	6] A 333							873

ctc tcc gag gag gtg cgc cag cga ctt cag gct ttc cgc cag gac acc Leu Ser Glu Glu Val Arg Gln Arg Leu Gln Ala Phe Arg Gln Asp Thr 280 . 285 . 290	921
tac ctg cag ata gct gcc ttc act cgc gcc atc gac cag gag act gag Tyr Leu Gln Ile Ala Ala Phe Thr Arg Ala Ile Asp Gln Glu Thr Glu 295 300 305	969
gag gtc cag cag ctg gcg cca cct cca cca ggc cac agt gcc ttc Glu Val Gln Gln Leu Ala Pro Pro Pro Pro Gly His Ser Ala Phe 310 315 320	1017
gcc cca gag ttt caa caa aca gac agt ggc aag gtt ctg agc aag ctg Ala Pro Glu Phe Gln Gln Thr Asp Ser Gly Lys Val Leu Ser Lys Leu 325 330 335	1065
cag gcc cgt ctg gat gac ctg tgg gaa gac atc act cac agc ctt cat Gln Ala Arg Leu Asp Asp Leu Trp Glu Asp Ile Thr His Ser Leu His 345 350 355	1113
gac cag ggc cac agc cat ctg ggg gac ccc tgaggatcta cctgcccagg Asp Gln Gly His Ser His Leu Gly Asp Pro 360 365	1163
cccattccca geteettgte tggggageet tggetetgag cetetageat ggtteagtee	1223
ttgaaagtgg cetgttgggt ggagggtgga aggteetgtg caggacaggg aggeeaceaa	1283
aggggctgct gtctcctgca tatccagect cctgcgactc cccaatctgg atgcattaca	1343
ttcaccaggc tttgcaaacc cagcctccca gtgctcattt gggaatgctc atgagttact	1403
ccattcaagg gtgagggagt agggagggag aggcaccatg catgtgggtg attatctgca	1463
agectgtttg cegtgatget ggaageetgt gecaetacat eetggagttt ggetetagte	1523
acttetgget geetggtgge caetgetaca getggteeae agagaggage aettgtetee	1583
ccagggctgc catggcagct atcaggggaa tagaagggag aaagagaata tcatggggag	1643
aacatgtgat ggtgtgtgaa tatccctgct ggctctgatg ctggtgggta cgaaaggtgt	1703
gggctgggat aagagagggc agagcccatg ttttctgaca taactctaca cctanataag	1763
ggactgaacc cttccaactg cgggagctcc ttaaaccctt ctggggagca tactgggggc	1823
tetteeccat etteagecee tteetetggg tteec	1858
<210> 2 <211> 366 <212> PRT	

<211> 366
<212> PRT
<213> Homo sapiens
<220>
<221> misc_feature
<222> (46)..(1143)

<223> n = a or c or g or t

<400> 2

Met Ala Ser Met Ala Ala Val Leu Thr Trp Ala Leu Ala Leu Leu Ser 1 10 15

Ala Phe Ser Ala Thr Gln Ala Arg Lys Gly Phe Trp Asp Tyr Phe Ser 20 25 30

Gln Thr Ser Gly Asp Lys Gly Arg Val Glu Gln Ile His Gln Gln Lys 35 40 45

Met Ala Arg Glu Pro Ala Thr Leu Lys Asp Ser Leu Glu Gln Asp Leu 50 60

Asn Asn Met Asn Lys Phe Leu Glu Lys Leu Arg Pro Leu Ser Gly Ser 65 70 75 80

Glu Ala Pro Arg Leu Pro Gln Asp Pro Val Gly Met Arg Arg Gln Leu 85 90 95

Gln Glu Glu Leu Glu Glu Val Lys Ala Arg Leu Gln Pro Tyr Met Ala 100 \$105\$

Glu Ala His Glu Leu Val Gly Trp Asn Leu Glu Gly Leu Arg Gln Gln . 115 120 125

Leu Lys Pro Tyr Thr Met Asp Leu Met Glu Gln Val Ala Leu Arg Val 130 140

Gln Glu Leu Gln Glu Gln Leu Arg Val Val Gly Glu Asp Thr Lys Ala 145 150 155 160

Gln Leu Leu Gly Gly Val Asp Glu Ala Trp Ala Leu Leu Gln Gly Leu 165 170 175

Gln Ser Arg Val Val His His Thr Gly Arg Phe Lys Glu Leu Phe His 180 185 190

Pro Tyr Ala Glu Ser Leu Val Ser Gly Ile Gly Arg His Val Gln Glu 195 200 205

Leu His Arg Ser Val Ala Pro His Ala Pro Ala Ser Pro Ala Arg Leu 210 215 220

Ser Arg Cys Val Gln Val Leu Ser Arg Lys Leu Thr Leu Lys Ala Lys 225 230 235 240

Ala Leu His Ala Arg Ile Gln Gln Asn Leu Asp Gln Leu Arg Glu Glu 245 250 255

Leu Ser Arg Ala Phe Ala Gly Thr Gly Thr Glu Glu Gly Ala Gly Pro $260 \hspace{1.5cm} 265 \hspace{1.5cm} 270 \hspace{1.5cm}$

Asp	Pro	Gln 275	Met	Leu	Ser	Glu	Glu 280	Val	Arg	Gln	Arg	Leu 285	Gln	Ala	Phe	
Arg	Gln 290	Asp	Thr	Tyr	Leu	Gln 295	Ile	Ala	Ala	Phe	Thr 300	Arg	Ala	Ile	Asp	
Gln 305	Glu	Thr	Glu	Glu	Val 310	Gln	Gln	Gln	Leu	Ala 315	Pro	Pro	Pro	Pro	Gly 320	
His	Ser	Ala	Phe	Ala 325	Pro	Glu	Phe	Gln	Gln 330	Thr	Asp	Ser	Gly	Lys 335	Val	
Leu	Ser	Lys	Leu 340	Gln	Ala	Arg	Leu	Asp 345	Asp	Leu	Trp	Glu	Asp 350	Ile	Thr	
His	Ser	Leu 355	His	Asp	Gln	Gly	His 360	Ser	His	Leu	Gly	Asp 365	Pro			
<210 <211 <212 <213	1> : 2> I	3 1425 DNA Homo	sapi	iens												
<220 <221 <222	1> (CDS (181)) ([1146)												
<400																
acc:		3	stata	raat t	-+ ++	- at ac	77727	- ca	aato	ract	teee	raas	>++ /	7200:	e ectaa	60
	aggag	gcc a												_	aactgg ccagcc	60 120
taga	aggaq actcq	gcc a	cagag	9999	aa go	catte	gtgt	c cta	ıgttç	gagg	ctaa	acagt	ca (gtato	aactgg ccagcc aggagg	
taga tcaa atg	aggag actcg acati gga	gee a gee t tea g	tgg	gggga aggca	aa go cc ca cag	catto agato ctc	gtgto cagco atc	c cta g tct aca	igtto gago agc	gagg ccag gtc	ctaa	acagt aacaa gtg	ca g	gtato acca: caa	aggagg aac	120
taga tcaa atg Met 1	aggag actog acath gga Gly cca	gec a gec t tea g tec ser	tgg tgg	gggga aggca gtg Val 5	aa go cc ca cag Gln gtg	catto agato ctc Leu gct	gtgtc cagcg atc Ile gga	g tota g tot aca Thr	agttogage agc ser 10	gagg ccag gtc Val caa	ctaa gcca ggg	acagt aacaa gtg Val	ca (cag Gln	gtato accas caa Gln 15	aggagg aac Asn	120 180
taga tcaa atg Met 1 cat His	aggagagactogacattagga gga Gly cca pro	gcc a gcc t tca g tcc ser ggc ggc gga	tgg Trp tgg Trp 20	gggga aggco gtg Val 5 aca Thr	cag Gln gtg Val	catto agato ctc Leu gct Ala	gtgtc cagcc atc Ile gga Gly	g tot aca Thr cag Gln 25	agtto agc ser 10 ttc Phe	gagg ccag gtc Val caa Gln	ctaa gcca ggg Gly gaa	acagt acagt gtg Val aag Lys	cag Gln aaa Lys 30	gtato accas caa Gln 15 cgc Arg	aggagg aac Asn ttc Phe	120 180 228
taga tcaa atg Met 1 cat His	aggagagactogacati gga gGly cca Pro gaa Glu	gcc a gcc t tca g tcc ser ggc gga Gly gaa Glu 35	tgg Trp tgg Trp 20 gtc Val	ggggaaggco gtg Val 5 aca Thr	cc cag Gln gtg Val gaa Glu act	catto agato ctc Leu gct Ala tac Tyr	gtgtc cagco atc Ile gga Gly ttc Phe 40	c cta g tct aca Thr cag Gln 25 cag Gln	agtto cgago agc Ser 10 ttc Phe aag Lys	gagg gtc Val caa Gln aaa Lys	gcca ggg gly gaa Glu	acagt acagt gtg Val aag Lys agc Ser 45	cag Gln aaa Lys 30 cca Pro	gtato accas caa Gln 15 cgc Arg gtg Val	aggagg aac Asn ttc Phe cat His	120 180 228 276
taga tcaa atg Met 1 cat His act Thr	aggagagagagagagagagagagagagagagagagaga	gcc a gcc t tca g tcc ser ggc ggaa Glu 35 atc Ile	tgg Trp tgg Trp 20 gtc Val ctg Leu	ggggaaggco gtg Val 5 aca Thr att Ile ctg Leu	cc cag Gln gtg Val gaa Glu act Thr	catto agato ctc Leu gct Ala tac Tyr agc Ser 55	gtgtc cagcc atc Ile gga Gly ttc Phe 40 gat Asp	aca Thr cag Gln 25 cag Gln gaa Glu	agtto gago agc Ser 10 ttc Phe aag Lys gcc Ala	gagg gtc Val caa Gln aaa Lys tgg Trp	gcca ggg Gly gaa Glu gtt Val aag Lys	acagt acagt acag yal aag Lys agc Ser 45 aga Arg	cag Gln aaa Lys 30 cca Pro ttc	gtato accas caa Gln 15 cgc Arg gtg Val gtg Val	ccagcc aggagg aac Asn ttc Phe cat His cgt Arg	120 180 228 276

	85	90	95
aaa gaa cag cag Lys Glu Gln Gln 100	Phe Arg Glu Trp l	tt ttg aaa gag ttt Phe Leu Lys Glu Phe 105	cct caa atc 516 Pro Gln Ile 110
aga tgg aag att Arg Trp Lys Ile 115	cag gag tcc ata g Gln Glu Ser Ile (120	gaa agg ctt cgt gtc Glu Arg Leu Arg Val 125	att gca aat 564 Ile Ala Asn
		ege gte ate gee aat Cys Val Ile Ala Asn 140	
		att ggc gtt atg ttg Ile Gly Val Met Leu 155	
		act gca gct ggg gta Fhr Ala Ala Gly Val 170	
	Thr Ala Gly Ile	gcc tcc agc atc gtg Ala Ser Ser Ile Val 185	
		gcc agc agg ctg act Ala Ser Arg Leu Thr 205	
		gac att ctg cat gac Asp Ile Leu His Asp 220	
	_	ttt gac gaa gcc aca Phe Asp Glu Ala Thr 235	-
		aga tct aaa gcc act Arg Ser Lys Ala Thr 250	
	Trp Arg Tyr Val	cct ata aat gtt gtt Pro Ile Asn Val Val 265	
		ata gtg aga aaa gta Ile Val Arg Lys Val 285	
		ctt gtt gtg ctg gat Leu Val Val Leu Asp 300	
		cac aag ggg gca aaa His Lys Gly Ala Lys 315	
gct gag tcgctga Ala Glu	ggc agtgggctca gg	agctggag gagaatctca	atgagctcac 1196
ccatatccat caga	gtctaa aagcaggcta	ggcccaattg ttgcggga	ag tcagggaccc 1256

caaacggagg	gactggctga	agccatggca	gaagaacgtg	gattgtgaag	atttcatgga	1316
catttattag	ttccccaaat	taatactttt	ataatttcct	atgcctgtct	ttaccgcaat	1376
ctctaaacac	caattgtgaa	gatttcatgg	acacttatca	cttccccaa		1425

<210> 4 <211> 322

<212> PRT

<213> Homo sapiens

<400> 4

Met Gly Ser Trp Val Gln Leu Ile Thr Ser Val Gly Val Gln Gln Asn 1 $$ 5 $$ 10 $$ 15

His Pro Gly Trp Thr Val Ala Gly Gln Phe Gln Glu Lys Lys Arg Phe 20 25 30

Thr Glu Glu Val Ile Glu Tyr Phe Gln Lys Lys Val Ser Pro Val His 35 40 45

Leu Lys Ile Leu Leu Thr Ser Asp Glu Ala Trp Lys Arg Phe Val Arg 50 55 60

Val Ala Glu Leu Pro Arg Glu Glu Ala Asp Ala Leu Tyr Glu Ala Leu 65 70 75 80

Lys Asn Leu Thr Pro Tyr Val Ala Ile Glu Asp Lys Asp Met Gln Gln 85 90 95

Lys Glu Gln Gln Phe Arg Glu Trp Phe Leu Lys Glu Phe Pro Gln Ile 100 \$105

Arg Trp Lys Ile Glu Ser Ile Glu Arg Leu Arg Val Ile Ala Asn 115 120 125

Glu Ile Glu Lys Val His Arg Gly Cys Val Ile Ala Asn Val Val Ser 130 135 140

Gly Ser Thr Gly Ile Leu Ser Val Ile Gly Val Met Leu Ala Pro Phe 145 150 155

Thr Ala Gly Leu Ser Leu Ser Ile Thr Ala Ala Gly Val Gly Leu Gly
165 170 175

Ile Ala Ser Ala Thr Ala Gly Ile Ala Ser Ser Ile Val Glu Asn Thr 180 185 190

Tyr Thr Arg Ser Ala Glu Leu Thr Ala Ser Arg Leu Thr Ala Thr Ser

Thr Asp Gln Leu Glu Ala Leu Arg Asp Ile Leu His Asp Ile Thr Pro

215 210 Asn Val Leu Ser Phe Ala Leu Asp Phe Asp Glu Ala Thr Lys Met Ile 235 230 225 Ala Asn Asp Val His Thr Leu Arg Arg Ser Lys Ala Thr Val Gly Arg 250 Pro Leu Ile Ala Trp Arg Tyr Val Pro Ile Asn Val Val Glu Thr Leu 260 Arg Thr Arg Gly Ala Pro Thr Arg Ile Val Arg Lys Val Ala Arg Asn Leu Gly Lys Ala Thr Ser Gly Val Leu Val Val Leu Asp Val Val Asn Leu Val Gln Asp Ser Leu Asp Leu His Lys Gly Ala Lys Ser Glu Ser 310 315 Ala Glu <210> 5 <211> 1931 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (18)..(452) gaagettete gaggace atg gaa ett gea etg etg tgt ggg etg gtg 50 Met Glu Leu Ala Leu Leu Cys Gly Leu Val Val atg gct ggt gtg att cca atc cag ggc ggg atc ctg aac ctg aac aag Met Ala Gly Val Ile Pro Ile Gln Gly Gly Ile Leu Asn Leu Asn Lys 98 15 atg gtc aag caa gtg act ggg aaa atg ccc atc ctc tcc tac tgg ccc 146 Met Val Lys Gln Val Thr Gly Lys Met Pro Ile Leu Ser Tyr Trp Pro tac ggc tgt cac tgc gga cta ggt ggc aga ggc caa ccc aaa gat gcc 194 Tyr Gly Cys His Cys Gly Leu Gly Gly Arg Gly Gln Pro Lys Asp Ala 45

acg gac tgg tgc tgc cag acc cat gac tgc tgc tat gac cac ctg aag

Thr Asp Trp Cys Cys Gln Thr His Asp Cys Cys Tyr Asp His Leu Lys

242

60	65	70	75
acc cag ggg tgc ggc Thr Gln Gly Cys Gly 80	atc tac aag gac tat Ile Tyr Lys Asp Tyr 85	tac aga tac aac tti Tyr Arg Tyr Asn Pho 90	t tcc 290 e Ser
cag ggg aac atc cac Gln Gly Asn Ile His 95	tgc tct gac aag gga Cys Ser Asp Lys Gly 100	agc tgg tgt gag cag Ser Trp Cys Glu Gl: 105	g cag 338 n Gln
ctg tgt gcc tgt gac Leu Cys Ala Cys Asp 110	aag gag gtg gcc ttc Lys Glu Val Ala Phe 115	tgc ctg aag cgc aa Cys Leu Lys Arg As 120	c ctg 386 n Leu
gac acc tac cag aag Asp Thr Tyr Gln Lys 125	cga ctg cgt ttc tac Arg Leu Arg Phe Tyr 130	tgg cgg ccc cac tg Trp Arg Pro His Cy 135	c cgg 434 s Arg
ggg cag acc cct ggg Gly Gln Thr Pro Gly 140	tgc tagaageeea cace Cys 145	ctctac cctgttcctc	482
agcatggagc tctggcat	cc ccacctcagt atctaa	cctg aaccagcctg gct	tttcaaa 542
cactccgggg ggaggtag	tc ccagcctccc ccggaa	ccct ctaccaatgc ctt	ctgacct 602
tctgaagctt tccgaatc	cct cccagttgag gcagta	gctg tgtcctctga ggg	tggatgg 662
gaatcttggg agaagcc	caa gcaagggagc cctcag	aggt ggtgtttgga cca	laagcatc 722
ggggtggggg aggggtct	gc cgctgtcccc cacctg	ctgg cccccttgtc ctt	cctcacc 782
ccctccaata tagtctcc	gga gctacaaccg cagcag	ccac tataaagggc aat	attgatc 842
tttctgtcca tgtggctc	cta tottttaaaa ootcaa	ggcc ctccactgtc cta	agataaa 902
gcctctcata ggcactgg	ggg accetgeaca gtetgg	ccat gtgaccctct ccc	ccaggcaa 962
gctctgaagt ccctgcag	ggt ggaggccatg cctgtc	ttaa actcagttgc atc	ccctggtg 1022
cccaaagcaa caccagaa	acc aagaaggagc tccata	aatc cttcttgggt gaa	agcctaga 1082
caaagccgcc aggtcttg	gtg gctccaggca ccagag	seett gagtaettte tee	etgeetee 1142
aggcattggc tcagggtg	gaa ttacaagggg ctactg	gaatg gctattactt tca	atcacgac 1202
tgatccccac ctcctcag	ggg tcaaagggct actttc	tgga agtetececa gg	etgactec 1262
ttctccctga ctgcaag	ggc tcactccctc ctccaa	agete ecacaatget te	atggctct 1322
gccgcttacc tagcttg	gcc tagagtggca aatgga	actt ctctgatctc cc	ccaactag 1382
actggagccc ccgaagg	atg gagaccatgt ctgtgo	cate tetgttteee et	gttttccc 1442
acatactagg tgctcaa	ttc atgcctgtga atggcg	ytgag cccataatgg at	acacagag 1502
gttgcagcag atggtgt	ggg tacctcaccc agatat	cette caggeecaag ge	ccctctcc 1562
ctgagtgagg ccaggtg	ttg gcagccaact gctcca	aatct geeteettee ee	taaatact 1622
gccctggtct agtggga	gct gccttccccc tgcccc	cacct ctcccaccaa ga	ggccacct 1682
gtcactcatg gccagga	gag tgacaccatg gagggt	tacaa ttgccagctc cc	ccgtgtct 1742

gtgcagcatt gtctgggttg aatgacact tcaaattgtt cctgggatcg ggctgaggcc 1802 aggcctctcc tggaaccacc tctctgcttg gtctgacccc ttggcctatc cagttttcct 1862 ggttccctca caggtttctc cagaaagtac tccctcagta aagcatttgc acaagaaaaa 1922 aaaaaaaaaa

<210> 6

<211> 145

<400> 6

Met Glu Leu Ala Leu Leu Cys Gly Leu Val Val Met Ala Gly Val Ile 1 5 10 15

Pro Ile Gln Gly Gly Ile Leu Asn Leu Asn Lys Met Val Lys Gln Val 20 25 30

Thr Gly Lys Met Pro Ile Leu Ser Tyr Trp Pro Tyr Gly Cys His Cys 35 40 45

Gly Leu Gly Gly Arg Gly Gln Pro Lys Asp Ala Thr Asp Trp Cys Cys 50 60

Gln Thr His Asp Cys Cys Tyr Asp His Leu Lys Thr Gln Gly Cys Gly 65 70 75 80

Ile Tyr Lys Asp Tyr Tyr Arg Tyr Asn Phe Ser Gln Gly Asn Ile His 85 90 95

Cys Ser Asp Lys Gly Ser Trp Cys Glu Gln Gln Leu Cys Ala Cys Asp 100 105 110

Lys Glu Val Ala Phe Cys Leu Lys Arg Asn Leu Asp Thr Tyr Gln Lys 115 120 125

Arg Leu Arg Phe Tyr Trp Arg Pro His Cys Arg Gly Gln Thr Pro Gly 130 135 140

Cys 145

<210> 7

<211> 1840

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (140)..(1840)

<400> 7 tcccgggtcg acgatttctt cctgatccca cagcatcgca gagctcggga ggcaca	agctc 60
acagacacag gaaacacagg actgctattc tgctctcctg cccacggtga tctggt	tgcca 120
gctggtggaa cagtgggtg atg gcg tcc ctg ctg caa gac cag ctg acc Met Ala Ser Leu Leu Gln Asp Gln Leu Thr 1	act 172 Thr
gat cag gac ttg ctg ctg atg cag gaa ggc atg ccg atg cgc aag c Asp Gln Asp Leu Leu Met Gln Glu Gly Met Pro Met Arg Lys v 15 20 25	gtg 220 Val
agg tcc aaa agc tgg aag aag cta aga tac ttc aga ctt cag aat q Arg Ser Lys Ser Trp Lys Lys Leu Arg Tyr Phe Arg Leu Gln Asn 30 35 40	gac 268 Asp
ggc atg aca gtc tgg cat gca cgg cag gcc agg ggc agt gcc aag Gly Met Thr Val Trp His Ala Arg Gln Ala Arg Gly Ser Ala Lys 45	ccc 316 Pro
agc ttc tca atc tct gat gtg gag aca ata cgt aat ggc cat gat Ser Phe Ser Ile Ser Asp Val Glu Thr Ile Arg Asn Gly His Asp 60 65 70	tcc 364 Ser 75
gag ttg ctg cgt agc ctg gca gag gag ctc ccc ctg gag cag ggc Glu Leu Leu Arg Ser Leu Ala Glu Glu Leu Pro Leu Glu Gln Gly 80 85 90	ttc 412 Phe
acc att gtc ttc cat ggc cgc cgc tcc aac ctg gac ctg atg gcc Thr Ile Val Phe His Gly Arg Arg Ser Asn Leu Asp Leu Met Ala 95 100 105	aac 460 Asn
agt gtt gag gag gcc cag ata tgg atg cga ggg ctc cag ctg ttg Ser Val Glu Glu Ala Gln Ile Trp Met Arg Gly Leu Gln Leu Leu 110 115 120	gtg 508 Val
gat ctt gtc acc agc atg gac cat cag gag cgc ctg gac caa tgg Asp Leu Val Thr Ser Met Asp His Gln Glu Arg Leu Asp Gln Trp 125 130 135	ctg 556 Leu
agc gat tgg ttt caa cgt gga gac aaa aat cag gat ggt aag atg Ser Asp Trp Phe Gln Arg Gly Asp Lys Asn Gln Asp Gly Lys Met 140 145 150	agt 604 Ser 155
ttc caa gaa gtt cag cgg tta ttg cac cta atg aat gtg gaa atg Phe Gln Glu Val Gln Arg Leu Leu His Leu Met Asn Val Glu Met 160 165 170	gac 652 Asp
caa gaa tat gcc ttc agt ctt ttt cag gca gca gac acg tcc cag Gln Glu Tyr Ala Phe Ser Leu Phe Gln Ala Ala Asp Thr Ser Gln 175 180 185	tct 700 Ser
gga acc ctg gaa gga gaa gaa ttc gta cag ttc tat aag gca ttg Gly Thr Leu Glu Gly Glu Glu Phe Val Gln Phe Tyr Lys Ala Leu 190 195 200	act 748 Thr
aaa cgt gct gag gtg cag gaa ctg ttt gaa agt ttt tca gct gat Lys Arg Ala Glu Val Gln Glu Leu Phe Glu Ser Phe Ser Ala Asp 205 210 215	ggg 796 Gly

cag Gln 220	aag Lys	ctg Leu	act Thr	ctg Leu	ctg Leu 225	gaa Glu	ttt Phe	ttg Leu	gat Asp	ttc Phe 230	ctc Leu	caa Gln	gag Glu	gag Glu	cag Gln 235	844
aag Lys	gag Glu	aga Arg	gac Asp	tgc Cys 240	acc Thr	tct Ser	gag Glu	ctt Leu	gct Ala 245	ctg Leu	gaa Glu	ctc Leu	att Ile	gac Asp 250	cgc Arg	892
tat Tyr	gaa Glu	cct Pro	tca Ser 255	gac Asp	agt Ser	ggc Gly	aaa Lys	ctg Leu 260	cgg Arg	cat His	gtg Val	ccg Pro	agt Ser 265	atg Met	gat Asp	940
ggc Gly	ttc Phe	ctc Leu 270	agc Ser	tac Tyr	ctc Leu	tgc Cys	tct Ser 275	aag Lys	gat Asp	gga Gly	gac Asp	atc Ile 280	ttc Phe	aac Asn	cca Pro	988
gcc Ala	tgc Cys 285	ctc Leu	ccc Pro	atc Ile	tat Tyr	cag Gln 290	gat Asp	atg Met	act Thr	caa Gln	ccc Pro 295	ctg Leu	aac Asn	cac His	tac Tyr	1036
ttc Phe 300	atc Ile	tgc Cys	tct Ser	tct Ser	cat His 305	aac Asn	acc Thr	tac Tyr	cta Leu	gtg Val 310	gly aaa	gac Asp	cag Gln	ctt Leu	tgc Cys 315	1084
ggc Gly	cag Gln	agc Ser	agc Ser	gtc Val 320	gag Glu	gga Gly	tat Tyr	ata Ile	cgg Arg 325	gcc Ala	ctg Leu	aag Lys	cgg Arg	330 Gly 399	tgc Cys	1132
cgc Arg	tgc Cys	gtg Val	gag Glu 335	gtg Val	gat Asp	gta Val	tgg Trp	gat Asp 340	gga Gly	cct Pro	agc Ser	Gly ggg	gaa Glu 345	cct Pro	gtc Val	1180
gtt Val	tac Tyr	cac His 350	gga Gly	cac His	acc Thr	ctg Leu	acc Thr 355	tcc Ser	cgc Arg	atc Ile	ctg Leu	ttc Phe 360	aaa Lys	gat Asp	gtc Val	1228
gtg Val	gcc Ala 365	aca Thr	gta Val	gca Ala	cag Gln	tat Tyr 370	gcc Ala	ttc Phe	cag G]n	aca Thr	tca Ser 375	gac Asp	tac Tyr	cca Pro	gtc Val	1276
Ile	Leu	tcc Ser	ctg Leu	gag Glu	Thr	His	tgc Cys	agc Ser	tgg Trp	gag Glu 390	Gln	cag Gln	cag Gln	acc Thr	atg Met 395	1324
gcc Ala	cgt Arg	cat His	ctg Leu	act Thr 400	Glu	atc Ile	ctg Leu	gly aaa	Glu	cag Gln	ctg Leu	ctg Leu	agc Ser	Thr	Thr	1372
ttg Leu	gat Asp	gly ggg	Val	Leu	ccc Pro	act Thr	cag Gln	Leu	Pro	tcg Ser	cct Pro	gag Glu	Glu	Leu	cgg Arg	1420
agg Arg	aag Lys	Ile	Leu	gtg Val	aag Lys	Gly 999	Lys	Lys	tta Leu	aca Thr	ctt Leu	Glu	Glu	gac Asp	ctg Leu	1468
gaa Glu	Tyr	Glu	gaa Glu	gag Glu	gaa Glu	Ala	Glu	. cct . Pro	gag Glu	ttg Leu	ı Glu	Glu	tca Ser	gaa Glu	ttg Leu	1516
Ala	Leu	gag Glu	tcc Ser	cag Gln	Phe	Glu	act Thr	gag Glu	cct Pro	Glu	ı Pro	cag Glr	gag Glu	g cag ı Glr	aac Asn 475	1564
	Gln 220 aag Lys tat Tyr ggcy gCly gCly cGly cGly cGly cGly cGly cGly cgcla tteu agg Arg galu gCla	aag gag Lys Glu tat gaa Tyr Glu ggc ttc Gly Phe gcc Ala Cys 285 ttc atc Phe 300 ggc tgc Arg Cys gtt tac Cys gtt tac Tyr gtg gcc Cys gtt tac Tyr gtg gcc Cys gtt tac Tyr gtg gcc Cys atc ttg Jeu 380 gcc cgt Ala Arg ttg gat Leu Asp agg aag Arg Lys gaa tat Glu Tyr	aag gag aga Lys Glu Arg tat gaa cct Tyr Glu Pro ggc ttc ctc Gly Phe Leu 270 gcc tgc ctc Ala Cys Leu 285 ttc atc tgc Phe Ile Cys 300 ggc cag agc Gly Gln Ser cgc tgc gtg Arg Cys Val gtt tac cac Val Tyr His 350 gtg gcc aca Val Ala Thr 365 atc ttg tcc Ile Leu Ser 380 gcc cgt cat Ala Arg His ttg gat ggg Leu Asp Gly agg aag atc Arg Lys Ile 430 gaa tat gag Glu Tyr Glu 445 gcg ctg gag Ala Leu Glu	Gln Lys Leu Thr 220 aag gag aga gac Lys Glu Arg Asp tat gaa cct tca Tyr Glu Pro Ser 255 ggc ttc ctc agc Gly Phe Leu Ser 270 gcc tgc ctc ccc Ala Cys Leu Pro 285 ttc atc tgc tct Phe Ile Cys Ser 300 ggc cag agc agc Gly Gln Ser Ser cgc tgc gtg gag Arg Cys Val Glu 335 gtt tac cac gga Val Tyr His Gly 350 gtg gcc aca gta Val Ala Thr 365 atc ttg tcc ctg Ile Leu Ser Leu 380 gcc cgt cat ctg Ala Arg His Leu ttg gat ggg gtg Leu Asp Gly Val agg aag atc Arg Lys Ile Leu Arg Lys Ile ctg Arg Lys Glu Glu gca ttg gag gag Glu Yal Ala Tyr Glu Glu Gaa tat gag gaa Glu Tyr Glu Glu Ser	aag gag aga gac tgc Lys Glu Arg Asp Cys 240 tat gaa cct tca gac Tyr Glu Pro Ser Asp 255 ggc ttc ctc agc tac Gly Phe Leu Ser Tyr 270 gcc tgc ctc ccc atc Phe Ile Cys Ser Ser 300 ggc tgc gtg agc gtg Arg Cys Val Glu Val 335 gtt tac cac gga cac Val Tyr His Gly His 365 atc ttg tcc ctg gag Ile Leu Ser Leu Glu 380 gcc cgt cat ctg gag Ile Leu Ser Leu Glu 380 gcc tgc gtg gtg gtg Arg Cys leu Ctg His act Ala Thr Val Ala 365 atc ttg tcc ctg gag Ile Leu Ser Leu Glu 380 gcc cgt cat ctg ctg Arg His Leu Thr 400 ttg gat ggg gtg ctg Leu Asp Gly Val Leu 415 agg aag atc ctg gag Glu Glu Glu gaa tat gag gaa gag Glu	Gin Lys Leu Thr Leu Leu 225 aag gag aga gac tgc acc Lys Glu Arg Asp Cys Thr 240 tat gaa cct tca gac agt Tyr Glu Pro Ser Asp Ser 255 ggc ttc ctc agc tac ctc Gly Phe Leu Ser Tyr Leu 270 gcc tgc ctc ccc atc tat Tyr 285 ttc atc tgc tct tct cat Cat Phe Ile Cys Ser Ser Val Glu 320 ggc tgc gtg gtg gag gtg gat Arg Cys Val Glu 320 cgc tgc gtg gtg gag gtg gat Arg Cys Val Glu 3320 cgc tgc gtg gtg gag gtg gat Arg Cys Val Glu 335 gtt tac cac gga cac acc Val Tyr His Gly His Thr 350 gtg gcc aca gta gca gca cag Val Ala Thr Val Ala Gln 365 atc ttg tcc ctg gag acc Ile Leu Ser Leu Glu Thr 380 gcc cgt cat ctg act gag Arg His Leu Thr Glu 400 ttg gat ggg gtg ctg ctg cag Arg Lys Ile Leu Val Leu Pro 415 agg aag atc ctg gtg gaa gac Gac acc Cag Arg Lys Ile Leu Val Lys 430 gaa tat gag gaa gaa gag gaa Gac Gac Cag Ctg Gag Glu	aag gag aga gac tgc acc tct Lys Glu Arg Asp Cys Thr Ser tat gaa cct tca gac agt ggc Tyr Glu Pro Ser Asp Ser Gly ggc ttc ctc agc tac ctc tgc Gly Phe Leu Ser Tyr Leu Cys 270 gcc tgc ctc ccc atc tat cag Ala Cys Leu Pro Ile Tyr Gln 285 ggc ttc atc tgc tct tct cat aac Phe Ile Cys Ser Ser His Asn 300 ggc tag agc agc gtc gag gga Gly Gln Ser Ser Val Glu Glu Gly 320 cgc tgc gtg gag gtg gat gat gta Arg Cys Val Glu Val Asp Val 335 gtt tac cac gga gag gtg gat gat Yal Tyr His Gly His Thr Leu 350 gtg gcc aca gga gag gtg acc ctg Val Tyr His Gly His Thr Leu 350 gtg gcc aca gga gag acc cac Yal Ala Thr Val Ala Gln Tyr 370 atc ttg tcc ctg gag acc cac Ile Leu Ser Leu Glu Thr His 380 gcc cgt cat ctg gag acc gag acc Ala Arg His Leu Thr Glu Ile 400 ttg gat ggg gtg ctg ctg acc Ala Arg His Leu Thr Glu Ile 400 gag aag acc Glu Tyr Glu Glu Ser Ctg Glu Tyr Glu 430 gaa tat gag gaa gaa gag gaa Glu Tyr Glu Glu Ser Gln Phe Glu 450	aag gag aga gac tgc acc tct gag Lys Glu Arg Asp Cys Thr Ser Glu tat gaa cct tca gac agt ggc aaa Tyr Glu Pro Ser Asp Ser Gly Lys ggc ttc ctc agc tac ctc tgc gag Cys Ser Asp Ser Gly Lys ggc ttc ctc agc tac ctc tgc tct Gly Phe Leu Ser Tyr Leu Cys Ser 270 gcc tgc ctc ccc atc tat cag gat Ala Cys Leu Pro Ile Tyr Gln Asp 305 ggc cag agc agc gtc gag gga tat Gly Gln Ser Ser His Asn Thr 300 ggc tgc gtg gag gtg gat gta tgg Arg Cys Val Glu Yal Asp 335 gtt tac cag gag cac acc ctg Ala Tyr His Gly His Thr Leu Thr 355 gtg gcc aca gta gca cac acc ctg Ala Thr Val Ala Gln Tyr Ala 365 gcc cgt cat ctg gag acc cac acc ctg Ala Arg His Leu Glu Thr Glu ttg gat gag gtg ctg ccc act ctg Arg Lys Ile Leu Val Lys Gly Lys A35 gaa tat gag gaa gag gaa gaa gca Glu Tyr Glu Glu Glu Thr A15 gcg ctg gag tcc cag ttt gag aac Arg Lys Ile Leu Val Lys Gly Lys A35 gcc ctg gag tcc cag ttt gag acc Arg Lys Ile Leu Val Lys Gly Lys A35 gca tat gag gaa gag gaa gaa gca gaa Glu Tyr Glu Glu Ser Gln Phe Glu Thr	aag gag aga aga ctgc acc tct gag ctt Lys Glu Arg Asp Cys Thr Ser Glu Leu tat gaa cct tca gac agt ggc aaa ctg Tyr Glu Pro Ser Asp Ser Gly Lys Leu 255 Asp Ser Gly Lys Leu 260 ggc ttc ctc agc tac ctc tgc Cys Ser Lys 270 gcc tgc ctc ccc atc tat cag gat atg Ala Cys Leu Pro Ile Tyr Glu Asp Met 281 ttc atc tgc tct tct cat aac acc tac Phe Ile Cys Ser Ser His Asn Thr Tyr 300 ggc cag agc ggt gag gtc gag gga tat ata Gly Gln Ser Ser Val Glu Gly Tyr Ile 320 cgc tgc gtg gtg gag gtg gat gta tgg gat Arg Cys Val Glu Asp 335 gtt tac cac gga gtg gat gta tgg gat Arg Cys Leu Pro Ile Thr Leu Thr Ser 355 gtg gcc aca gga gga gat gta gat Arg Cys Val Glu Ala Glu Gly Tyr Ala Phe 365 gtg gcc aca gta gta gad acc ctc Val Tyr His Gly His Thr Leu Thr Ser 380 gcc cgt cat ctg act gag acc cac tgc Ile Leu Ser Leu Glu Thr Glu ttg gat ggg gtg ctg ctg cac acc tgc Ala Arg His Leu Thr Glu Ile Leu Gly 415 acg aag acg atc ctg gtg gag gaa gca aag Arg Lys Ile Leu Val Lys Gly Lys 430 gca tat gag gaa gaa gaa gca gaa acc gaa ctg cat cac cag acc gaa aag atc ctg gtg aag gaa gca aag Arg Lys Ile Leu Val Lys Gly Lys 430 gcg ctg gag ttc cag gaa gca gaa acc gaa ctg gag ctg gag gaa gca gaa acc gaa aag atc ctg gtg aag gaa gca gaa acc gaa tat gag gaa gaa gca gaa acc gaa ctg gag ttc ggt aag gaa gca gaa acc gaa ctg gag ttc ggt aag gaa gca gaa acc gaa ctg gag acc gaa tat gag gaa gaa gaa gca gaa acc gaa tat gag gaa gaa gaa gca gaa acc gaa tat gag gaa gaa gaa gca gaa acc gaa tat gag gaa gaa gaa gaa gaa acc gaa tat gag gaa gaa gaa gaa gaa acc gaa tat gag gaa gaa gaa gaa gaa acc gaa tat gag gaa gaa gaa gaa gaa acc gaa tat gag gaa gaa gaa gaa acc gac ctg gag tcc caa ttg gag aag atc ctg gag aag gaa gaa gaa acc gaa tat gag gaa gaa gaa gaa acc gaa tat gag gaa gaa gaa gaa acc gaa tat gag gaa gaa gaa gaa gaa acc gaa tat gag gaa gaa gaa gaa acc gaa ctg gag ctg gaa gaa gaa gaa acc gaa tat gag gaa gaa gaa gaa gaa acc gaa tat gag gaa gaa gaa gaa gaa acc gaa ctg ctg gag tcc caa ttg gag aa tat gag gaa gaa gaa gaa gaa gaa acc gaa ctg ctg gag tcc caa ttg gag aa tat gag gaa ga	Gln Lys Leu Thr Leu Leu Leu Glu Phe Leu Asp 220 aag gag gac tys acc tct gag ctt gct Lys Glu Pro Ser Asp Cys Thr Ser Glu Leu Asp gag ctt tca gag agc agc agc agg a	Gln Lys Leu Thr Leu Leu Glu Phe Leu Asp Phe 220 230 aag aga aga tet 225 Glu Phe Leu Asp Phe Lys Glu Arg Asp Cys Thr Ser Glu Leu Asla Leu tat gaa ct toa agt agt ggc aaa ctg cgg cat ggc ttc ctc agc tac ctc tys Asp Gly Asp Asp Asp Asp Gly Asp Asp	Gin Lys Leu Thr Leu Leu Cau Glu Phe Leu Asp Phe Leu Phe Leu 230 aag gag agag agag agag Lys du Arg Asp Cys Thr Ser Glu Leu Ala Cau Gut Gut	Gin Lys Leu Thr Leu Leu Glu Phe Leu Asp Phe Leu Gln 220 aag gag aga gac tgc acc tct gag ctt get ctg gaa ctc Lys Glu Arg Asp Cys Thr Ser Glu Leu Ala Leu Glu Leu 245 tat gaa cct tca gac agt ggc aaa ctg cgg cat gtg ccg Tyr Glu Pro Ser Asp Ser Gly Lys Leu Arg His Val Pro 255 ggc ttc ctc agc tac ctc tgc tct aag gat gga gac atc Gly Phe Leu Ser Tyr Leu Cys Ser Lys Asp Gly Asp Ile 270 gcc tgc ctc ccc atc tat cag gat atg act caa ccc ctg Ala Cys Leu Pro Ile Tyr Glu Asp Met Thr Glu Pro Leu 295 ttc atc tgc tct tct cat aac acc tac gtg ggg gac gly Gly Gly Eys Ser Ser His Asn Thr Tyr Leu Val Gly Asp 300 ggc cag agc agc gtg gag gtg gat gta tat ata cag ggg gac ctg agg gac gly Gly Gly Eys Asp Gly Pro Ser Gly Gly Fro Ser Gly Ser Ser Val Glu Gly Tyr Ile Arg Ala Leu Lys 320 ggc tgc gtg gag gtg gat gta tat ata cag gga cct agc ggg gac Arg Cys Val Gly Wal Asp 320 ggt tac cac gga cac acc ctg acc tac cac ctg acc gag gga his Ser Ser Wal Gly Wal Asp 320 ggt tac cac gga cac acc ctg acc ctg acc tac cac ctg acc gag gga his Ser Arg Ile Leu Lys 320 ggt gcc gtg gag gtg gat gtg	Cin Lys Leu Thr Leu Leu Glu Phe Leu Asp Phe Leu Glu Glu 220 225	Gin Lys Leu Thr Leu Leu Glu Phe Leu Asp Phe Leu Glu Glu Glu 225 230 230 230 230 aga aga aga gag aga type acc tet gag ctt get etg gaa ctc att gac Lys Glu Arg Asp Cys Thr Ser Glu Leu Ala Leu Glu Leu Ile Asp 245 245 255 255 255 257 259 250 250 250 250 250 250 250 250 250 255 255	aag gag aga gac gac bet gag ctt get ctg gaa ctt att gac cgc lys Glu Arg Asp Cys Thr Ser Glu Leu Ala Leu Glu Leu IIe Asp Arg 240 tat gaa cct tca gac agt ggc aaa ctg cgg cat gtg ccg agt atg gat Tyr Glu Pro Ser Asp Ser Gly Lys Leu Arg His Val Pro Ser Met Asp 260 ggc ttc ctc agc tac ctc tgc tct aag gat gga gac atc ttc aac cac Gly Phe Leu Ser Tyr Leu Cys Ser Lys Asp Gly Asp IIe Phe Asn Pro 280 ggc tgc ctc ccc atc tat cag gat atg gat gat gat gat gat gat lie Phe Asn Pro 280 ggc tgc ctc ccc atc tat cag gat atg act caa ccc ctg aac cac tac Ala Cys Leu Pro IIe Tyr Glu Asp Met Thr Gln Pro Leu Asn His Tyr 285 ttc atc tgc tct tct cat aac acc tac cta gtg ggg gac cac ct tgc Phe IIe Cys Ser Ser His Asn Thr Tyr Leu Val Gly Asp Gln Leu Cys 300 ggc cag agc agc gtc gag ggs tat at atc cgg gcc ctg aag cgg ggg tgc Gly Gln Ser Ser Val Glu Gly Tyr IIe Arg Ala Leu Lys Arg Gly Cys 320 cgc tgc gtg gag gtg gat gta tgg gga gac gag cct agc ggg gag cag cag ctg gag gag gac gag ctg gag gac ctg gag gag gac act gta gag gar cag ctg gag gac gag ctg gag gac ctg gag gac ctg gag gac ctg gag gac cag ctg gag gac gac act gta Ala Cys 330 ggt tac cac gga gat gta gta tgg gat gga cct agc ggg gac ctg gag cag ctg gag ctg gac ctg gag gac ctg gag cag ctg gag ctg gac ctg gag gac ctg gag gac ctg gag cag ctg gag ctg gac ctg gag gac cag gac cag gac gac gac gac ga

ctt Leu	cag Gln	aat Asn	aag Lys	gac Asp 480	aaa Lys	aag Lys	aag Lys	aaa Lys	tcc Ser 485	aag Lys	ccc Pro	atc Ile	ttg Leu	tgt Cys 490	cca Pro	1612
gcc Ala	ctc Leu	tct Ser	tcc Ser 495	ctg Leu	gtt Val	atc Ile	tac Tyr	ttg Leu 500	aag Lys	tct Ser	gtc Val	tca Ser	ttc Phe 505	cgc Arg	agc Ser	1660
ttc Phe	aca Thr	cat His 510	tca Ser	aag Lys	gag Glu	cac His	tac Tyr 515	cac His	ttc Phe	tac Tyr	gag Glu	ata Ile 520	tca Ser	tct Ser	ttc Phe	1708
tct Ser	gaa Glu 525	acc Thr	aag Lys	gcc Ala	aag Lys	cgc Arg 530	ctc Leu	atc Ile	aag Lys	gag Glu	gct Ala 535	ggc Gly	aat Asn	gag Glu	ttt Phe	1756
gtg Val 540	cag Gln	cac His	aat Asn	act Thr	cgg Arg 545	cag Gln	tta Leu	agc Ser	cgt Arg	gtg Val 550	tat Tyr	ccc Pro	agc Ser	ggc Gly	ctg Leu 555	1804
agg Arg	aca Thr	ggc Gly	tct Ser	tcc Ser 560	atc Ile	tac Tyr	aac Asn	ccg Pro	cag Gln 565	gga Gly	tac Tyr					1840
<21 <21 <21	1> ! 2> !	8 567 PRT														
<21	3>]	Homo	sap.	iens												
<40		8														
Met 1	Ala	Ser	Leu	Leu 5	Gln	Asp	Gln	Leu	Thr 10	Thr	Asp	Gln	Asp	Leu 15	Leu	
Leu	. Met	Gln	Glu 20	Gly	Met	Pro	Met	Arg 25	Lys	Val	Arg	Ser	Lys 30	Ser	Trp	
Lys	Lys	Leu 35	Arg	Tyr	Phe	Arg	Leu 40	Gln	Asn	Asp	Gly	Met 45	Thr	Val	Trp	
His	Ala 50	Arg	Gln	Ala	Arg	Gly 55	Ser	Ala	Lys	Pro	Ser 60	Phe	Ser	Ile	Ser	
Asp 65	Val	Glu	Thr	Ile	Arg 70	Asn	Gly	His	Asp	Ser 75	Glu	Leu	Leu	Arg	Ser 80	
Leu	ı Ala	Glu	Glu	Leu 85	Pro	Leu	Glu	Gln	Gly 90	Phe	Thr	Ile	Val	Phe 95	His	
GlΣ	/ Arg	Arg	Ser 100		Leu	Asp	Leu	Met 105		Asn	Ser	Val	Glu 110		Ala	
Glr	n Ile	: Trp		Arg	Gly	Leu	Gln 120		Leu	Val	Asp	Leu 125		Thr	Ser	

Met Asp His Gln Glu Arg Leu Asp Gln Trp Leu Ser Asp Trp Phe Gln 130 135 140

Arg Gly Asp Lys Asn Gln Asp Gly Lys Met Ser Phe Gln Glu Val Gln 145 150 155 160

Arg Leu Leu His Leu Met Asn Val Glu Met Asp Gln Glu Tyr Ala Phe 165 170 175

Ser Leu Phe Gln Ala Ala Asp Thr Ser Gln Ser Gly Thr Leu Glu Gly
180 185 190

Glu Glu Phe Val Gln Phe Tyr Lys Ala Leu Thr Lys Arg Ala Glu Val 195 200 205

Gln Glu Leu Phe Glu Ser Phe Ser Ala Asp Gly Gln Lys Leu Thr Leu 210 215 220

Leu Glu Phe Leu Asp Phe Leu Gln Glu Glu Gln Lys Glu Arg Asp Cys 225 230 235 235

Thr Ser Glu Leu Ala Leu Glu Leu Ile Asp Arg Tyr Glu Pro Ser Asp 245 250 255

Ser Gly Lys Leu Arg His Val Pro Ser Met Asp Gly Phe Leu Ser Tyr 260 265 270

Leu Cys Ser Lys Asp Gly Asp Ile Phe Asn Pro Ala Cys Leu Pro Ile 275 280 285

Tyr Gln Asp Met Thr Gln Pro Leu Asn His Tyr Phe Ile Cys Ser Ser 290 295 300

His Asn Thr Tyr Leu Val Gly Asp Gln Leu Cys Gly Gln Ser Ser Val 305 310 315 320

Glu Gly Tyr Ile Arg Ala Leu Lys Arg Gly Cys Arg Cys Vai Glu Val 325 330 335

Asp Val Trp Asp Gly Pro Ser Gly Glu Pro Val Val Tyr His Gly His 340 345 350

Thr Leu Thr Ser Arg Ile Leu Phe Lys Asp Val Val Ala Thr Val Ala 355 360

Gln Tyr Ala Phe Gln Thr Ser Asp Tyr Pro Val Ile Leu Ser Leu Glu 370 375 380 Thr His Cys Ser Trp Glu Gln Gln Gln Thr Met Ala Arg His Leu Thr

385 395 Glu Ile Leu Gly Glu Gln Leu Leu Ser Thr Thr Leu Asp Gly Val Leu 405 410 Pro Thr Gln Leu Pro Ser Pro Glu Glu Leu Arg Arg Lys Ile Leu Val 425 Lys Gly Lys Lys Leu Thr Leu Glu Glu Asp Leu Glu Tyr Glu Glu Glu 440 435 Glu Ala Glu Pro Glu Leu Glu Glu Ser Glu Leu Ala Leu Glu Ser Gln Phe Glu Thr Glu Pro Glu Pro Gln Glu Gln Asn Leu Gln Asn Lys Asp 480 465 470 Lys Lys Lys Ser Lys Pro Ile Leu Cys Pro Ala Leu Ser Ser Leu 485 490 Val Ile Tyr Leu Lys Ser Val Ser Phe Arg Ser Phe Thr His Ser Lys 505 500 Glu His Tyr His Phe Tyr Glu Ile Ser Ser Phe Ser Glu Thr Lys Ala 515 Lys Arg Leu Ile Lys Glu Ala Gly Asn Glu Phe Val Gln His Asn Thr 530 535 540 Arg Gln Leu Ser Arg Val Tyr Pro Ser Gly Leu Arg Thr Gly Ser Ser 545 550 555 Ile Tyr Asn Pro Gln Gly Tyr 565 <210> 9 <211> 1384 <212> DNA <213> Homo sapiens <400> 9 60 ccaactaagc ttgcctaatt tgcttcagaa ttggaagagg gaattgcagc aggaaaatat gtgaagagtt tttaaaccca caaattcttc ttactttaga attagttgtt acattggcag 120 180 gaaaaaataa atgcagatgt tggaccatgt tggaaacctt gtcaagacag tggattgtct cacacagaat ggaaatgtgg cttctgattc tggtggcgta tatgttccag agaaatgtga 240

attcagtaca tatgccaact aaagctgtgg acccagaagc attcatgaat attagtgaaa

300

tcatccaaca tcaaggctat c	cctgtgagg aatatgaagt	cgcaactgaa gatgggtata	360
tcctttctgt taacaggatt c	ctcgaggcc tagtgcaacc	taagaagaca ggttccaggc	420
ctgtggtgtt actgcagcat g	gcctagttg gaggtgctag	caactggatt tccaacctgc	480
ccaacaatag cctgggcttc a	attctggcag atgctggttt	tgacgtgtgg atggggaaca	540
gcaggggaaa cgcctggtct c	gaaaacaca agacactctc	catagaccaa gatgagttct	600
gggctttcag ttatgatgag a	atggctaggt ttgaccttcc	tgcagtgata aactttattt	660
tgcagaaaac gggccaggaa a	agatctatt atgtcggcta	ttcacagggc accaccatgg	720
gctttattgc atittccacc a	atgccagagc tggctcagaa	aatcaaaatg tattttgctt	780
tagcacccat agccactgtt a	agcatgcaa aaagccccgg	gaccaaattt ttgttgctgc	840
cagatatgat gatcaaggga t	tgtttggca aaaaagaatt	tctgtatcag accagatttc	900
tcagacaact tgttatttac c	ctttgtggcc aggtgattct	tgatcagatt tgtagtaata	960
tcatgttact tctgggtgga t	tcaacacca acaatatgaa	catgagccga gcaagtgtat	1020
atgctgccca cactcttgct g	ggaacatctg tgcaaaatat	tctacactgg agccaggcag	1080
tgaattctgg tgaactccgg g	gcatttgact gggggagtga	gaccaaaaat ctggaaaaat	1140
gcaatcagcc aactcctgta a	aggtacagag tcagagatat	gacggtccct acagcaatgt	1200
ggacaggagg tcaggactgg c	ctttcaaatc cagaagacgt	gaaaatgctg ctctctgagg	1260
tgaccaacct catctaccat a	aagaatattc ctgaatgggc	tcatgtggat ttcatctggg	1320
gtttggatgc tcctcaccgt a	atgtacaatg aaatcatcca	tctgatgcag caggaggaga	1380
ccat			1384
<210> 10 <211> 1915 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (180)(1046)			
<400> 10 ccgcacgagg gaaagaacat t	taggaatgcc ttttagtgcc	ttgcttcctg aactagctca	60
cagtageceg geggeecagg	gcaatccgac cacatttcac	tctcaccgct gtaggaatcc	120
agatgcaggc caagtacagc a	agcacgaggg acatgctgga	tgatgatggg gacaccacc	179
atg agc ctg cat tct cas Met Ser Leu His Ser Glr 1 5			227
cgg cgc aca gag cac agg Arg Arg Thr Glu His Arg 20	g gct ccc tct tca acg g Ala Pro Ser Ser Thr 25	tgg cga cca gtg gcc Trp Arg Pro Val Ala 30	275

ctg Leu	acc Thr	ctg Leu 35	ctg Leu	act Thr	ttg Leu	tgc Cys	ttg Leu 40	gtg Val	ctg Leu	ctg Leu	ata Ile	999 Gly 45	ctg Leu	gca Ala	gcc Ala	323
ctg Leu	999 Gly 50	ctt Leu	ttg Leu	ttt Phe	ttt Phe	cag Gln 55	tac Tyr	tac Tyr	cag Gln	ctc Leu	tcc Ser 60	aat Asn	act Thr	ggt Gly	caa Gln	371
gac Asp 65	acc Thr	att Ile	tct Ser	caa Gln	atg Met 70	gaa Glu	gaa Glu	aga Arg	tta Leu	gga Gly 75	aat Asn	acg Thr	tcc Ser	caa Gln	gag Glu 80	419
ttg Leu	caa Gln	tct Ser	ctt Leu	caa Gln 85	gtc Val	cag Gln	aat Asn	ata Ile	aag Lys 90	ctt Leu	gca Ala	gga Gly	agt Ser	ctg Leu 95	cag Gln	467
cat His	gtg Val	gct Ala	gaa Glu 100	aaa Lys	ctc Leu	tgt Cys	cgt Arg	gag Glu 105	ctg Leu	tat Tyr	aac Asn	aaa Lys	gct Ala 110	gga Gly	ggc Gly	515
tat Tyr	aca Thr	aga Arg 115	aac Asn	atg Met	gtg Val	cca Pro	gca Ala 120	tct Ser	gct Ala	tct Ser	tct Ser	gag Glu 125	agc Ser	ctc Leu	agg Arg	563
cag Gln	ctt Leu 130	cca Pro	cac His	atg Met	Gly 333	gaa Glu 135	agt Ser	gca Ala	gca Ala	gca Ala	cac His 140	agg Arg	tgc Cys	agc Ser	cct Pro	611
tgt Cys 145	aca Thr	gaa Glu	caa Gln	tgg Trp	aaa Lys 150	tgg Trp	cat His	gga Gly	gac Asp	aat Asn 155	tgc Cys	tac Tyr	cag Gln	ttc Phe	tat Tyr 160	659
aaa Lys	gac Asp	agc Ser	aaa Lys	agt Ser 165	tgg Trp	gag Glu	gac Asp	tgt Cys	aaa Lys 170	tat Tyr	ttc Phe	tgc Cys	ctt Leu	agt Ser 175	gaa Glu	707
aac Asn	tct Ser	acc Thr	atg Met 180	ctg Leu	aag Lys	ata Ile	aac Asn	aaa Lys 185	caa Gln	gaa Glu	gac Asp	ctg Leu	gaa Glu 190	ttt Phe	gcc Ala	755
gcg Ala	tct Ser	cag Gln 195	Ser	tac Tyr	tct Ser	gag Glu	ttt Phe 200	Phe	tac Tyr	tct Ser	tat Tyr	tgg Trp 205	Thr	gly	ctt Leu	803
ttg Leu	cgc Arg 210	Pro	gac Asp	agt Ser	ggc	aag Lys 215	gcc Ala	tgg Trp	ctg Leu	tgg Trp	atg Met 220	Asp	gga Gly	acc Thr	cct Pro	851
ttc Phe 225	Thr	tct Ser	gaa Glu	ctg Leu	ttc Phe 230	His	att Ile	ata : Ile	ata Ile	gat Asp 235	Val	acc Thr	ago Ser	cca Pro	aga Arg 240	899
ago Ser	aga Arg	gac Asp	tgt Cys	gtg Val 245	Ala	atc Ile	ctt Leu	aat Asn	999 Gly 250	Met	atc Ile	tto Phe	tca Ser	aag Lys 255	gac Asp	947
tgc Cys	aaa Lys	gaa Glu	ttg Leu 260	Lys	cgt Arg	tgt Cys	gto Val	tgt Cys 265	Glu	aga Arg	ago Aro	gca Ala	gga Gly 270	/ Met	gtg : Val	995
aag Lys	g cca	gag Glu 275	ı Ser	cto Leu	cat His	gtc Val	280	Pro	gaa Glu	aca Thr	tta Leu	ggc Gl _y 285	glı,	ı ggt ı Gl _y	gac Asp	1043

tga ttcgccct	ct gcaacta	caa atagcag	agt gagccaç	ggg gtgccaa	agc	1096
aagggctagt t	tgagacattg	ggaaatggaa	cataatcagg	aaagactatc	tctctgacta	1156
gtacaaaatg g	ggttctcgtg	tttcctgttc	aggatcacca	gcatttctga	gcttgggttt	1216
atgcacgtat t	ttaacagtca	caagaagtct	tatttacatg	ccaccaacca	acctcagaaa	1276
cccataatgt o	catctgcctt	cttggcttag	agataacttt	tagctctctt	tcttctcaat	1336
gtctaatatc a	acctccctgt	tttcatgtct	tccttacact	tggtggaata	agaaactttt	1396
tgaagtagag (gaaatacatt	gaggtaacat	ccttttctct	gacagtcaag	tagtccatca	1456
gaaattggca	gtcacttccc	agattgtacc	agcaaataca	caaggaattc	tttttgtttg	1516
tttcagttca	tactagtccc	ttcccaatcc	atcagtaaag	accccatctg	ccttgtccat	1576
gccgtttccc	aacagggatg	tcacttgata	tgagaatctc	aaatctcaat	gccttataag	1636
cattccttcc	tgtgtccatt	aagactctga	taattgtctc	ccctccatag	gaatttctcc	1696
caggaaagaa	atatatcccc	atctccgttt	catatcagaa	ctaccgtccc	cgatattccc	1756
ttcagagaga	ttaaagacca	gaaaaaaggg	gggctttttt	tttgcacctg	taatagtttc	1816
cggtcctttt	ttttttcctt	gacccctttt	ttttcccttc	cgggggtgga	gggtttatta	1876
taattaaagg	gaataccggg	qaaaaaaaa	aaaaagggg			1915

<210> 11

<211> 288

<212> PRT

<213> Homo sapiens

<400> 11

Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr Arg His Pro Glu Pro 1 5 10 15

Arg Arg Thr Glu His Arg Ala Pro Ser Ser Thr Trp Arg Pro Val Ala 20 25 30

Leu Thr Leu Leu Thr Leu Cys Leu Val Leu Leu Ile Gly Leu Ala Ala 35 40 45

Leu Gly Leu Leu Phe Phe Gln Tyr Tyr Gln Leu Ser Asn Thr Gly Gln 50 55 60

Asp Thr Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr Ser Gln Glu 65 70 75 80

Leu Gln Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly Ser Leu Gln 85 90 95

His Val Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys Ala Gly Gly

Tyr Thr Arg Asn Met Val Pro Ala Ser Ala Ser Ser Glu Ser Leu Arg 115 120 125

Gln Leu Pro His Met Gly Glu Ser Ala Ala Ala His Arg Cys Ser Pro 130 135 140

Cys Thr Glu Gln Trp Lys Trp His Gly Asp Asn Cys Tyr Gln Phe Tyr 145 150 155 160

Lys Asp Ser Lys Ser Trp Glu Asp Cys Lys Tyr Phe Cys Leu Ser Glu 165 170 175

Asn Ser Thr Met Leu Lys Ile Asn Lys Gln Glu Asp Leu Glu Phe Ala 180 185 190

Ala Ser Gln Ser Tyr Ser Glu Phe Phe Tyr Ser Tyr Trp Thr Gly Leu 195 200 205

Leu Arg Pro Asp Ser Gly Lys Ala Trp Leu Trp Met Asp Gly Thr Pro 210 215 220

Phe Thr Ser Glu Leu Phe His Ile Ile Ile Asp Val Thr Ser Pro Arg 225 230 235 240

Ser Arg Asp Cys Val Ala Ile Leu Asn Gly Met Ile Phe Ser Lys Asp 245 250 255

Cys Lys Glu Leu Lys Arg Cys Val Cys Glu Arg Arg Ala Gly Met Val 260 265 270

Lys Pro Glu Ser Leu His Val Pro Pro Glu Thr Leu Gly Glu Gly Asp 275 280 285

<210> 12

<211> 2420

<212> DNA

<213> Homo sapiens

<220>

Marie Contraction of the Contrac

And make

Man Man

T

<221> misc_feature

 $\langle 223 \rangle$ n = a or c or g or t

<220>

<221> CDS

<222> (200)..(2395)

<223> Xaa = Unknown or other

<400> 12 cgggaggaat ggaaggagaa ggcggaatgt gggagggctc agggggatgt gggagggacg	60
aacggagaag ggggagagag gggggtccag tctcccctgg ccgagcattt ttttttttg	120
gaagteetag gaetaatete caggaecage actettetee cagecettag ggteetgete	180
ggccaaggcc ttccctgcc atg cga cct gtc agt gtc tgg cag tgg agc ccc Met Arg Pro Val Ser Val Trp Gln Trp Ser Pro 1 5 10	232
tgg ggg ctg ctg ctg tgc ctg ctg tgc agt tcg tgc ttg ggg tct ccg Trp Gly Leu Leu Cys Leu Leu Cys Ser Ser Cys Leu Gly Ser Pro 15 20 25	280
tcc cct tcc acg ggc cct gag aag aag gcc ggg agc cag ggg ctt cgg Ser Pro Ser Thr Gly Pro Glu Lys Lys Ala Gly Ser Gln Gly Leu Arg 30 35	328
ttc cgg ctg gct ggc ttc ccc agg aag ccc tac gag ggc cgc gtg gag Phe Arg Leu Ala Gly Phe Pro Arg Lys Pro Tyr Glu Gly Arg Val Glu 45	376
ata cag cga gct ggt gaa tgg ggc acc atc tgc gat gat gac ttc acg Ile Gln Arg Ala Gly Glu Trp Gly Thr Ile Cys Asp Asp Asp Phe Thr 60 65 70 75	424
ctg cag gct gcc cac atc ctc tgc cgg gag ctg ggc ttc aca gag gcc Leu Gln Ala Ala His Ile Leu Cys Arg Glu Leu Gly Phe Thr Glu Ala 80 85 90	472
aca ggc tgg acc cac agt gcc aaa tat ggc cct gga aca ggc cgc atc Thr Gly Trp Thr His Ser Ala Lys Tyr Gly Pro Gly Thr Gly Arg Ile 95 100 105	520
tgg ctg gac aac ttg agc tgc agt ggg acc gag cag agt gtg act gaa Trp Leu Asp Asn Leu Ser Cys Ser Gly Thr Glu Gln Ser Val Thr Glu 110 115 120	568
tgt gcc tcc cgg ggc tgg ggg aac agt gac tgt acg cac gat gag gat Cys Ala Ser Arg Gly Trp Gly Asn Ser Asp Cys Thr His Asp Glu Asp 125 130 135	616
gct ggg gtc atc tgc aaa gac cag cgc ctc cct ggc ttc tcg gac tcc Ala Gly Val Ile Cys Lys Asp Gln Arg Leu Pro Gly Phe Ser Asp Ser 140 145 150 155	664
aat gtc att gag gta gag cat cac ctg caa gtg gag gag gtg cga att Asn Val Ile Glu Val Glu His His Leu Gln Val Glu Glu Val Arg Ile 160 165 170	712
cga ccc gcc gtt ggg tgg ggc aga cga ccc ctg ccc gtg acg gag ggg Arg Pro Ala Val Gly Trp Gly Arg Arg Pro Leu Pro Val Thr Glu Gly 175 180 185	760
ctg gtg gaa gtc agg ctt cct gac ggc tgg tcg caa gtg tgc gac aaa Leu Val Glu Val Arg Leu Pro Asp Gly Trp Ser Gln Val Cys Asp Lys 190 195 200	808
ggc tgg agc gcc cac aac agc cac gtg gtc tgc ggg atg ctg ggc ttc Gly Trp Ser Ala His Asn Ser His Val Val Cys Gly Met Leu Gly Phe 205 210 215	856

ccc Pro 220	agc Ser	gaa Glu	aag Lys	agg Arg	gtc Val 225	aac Asn	gcg Ala	gcc Ala	ttc Phe	tac Tyr 230	agg Arg	ctg Leu	cta Leu	gcc Ala	caa Gln 235	904
cgg Arg	cag Gln	caa Gln	cac His	tcc Ser 240	ttt Phe	ggt Gly	ctg Leu	cat His	999 Gly 245	gtg Val	gcg Ala	tgc Cys	gtg Val	ggc Gly 250	acg Thr	952
gag Glu	gcc Ala	cac His	ctc Leu 255	tcc Ser	ctc Leu	tgt Cys	tcc Ser	ctg Leu 260	gag Glu	ttc Phe	tat Tyr	cgt Arg	gcc Ala 265	aat Asn	gac Asp	1000
acc Thr	gcc Ala	agg Arg 270	tgc Cys	cct Pro	gly ggg	gly aaa	ggc Gly 275	cct Pro	gca Ala	gtg Val	gtg Val	agc Ser 280	tgt Cys	gtg Val	cca Pro	1048
ggc Gly	cct Pro 285	gtc Val	tac Tyr	gcg Ala	gca Ala	tcc Ser 290	agt Ser	ggc Gly	cag Gln	aag Lys	aag Lys 295	caa Gln	caa Gln	cag Gln	tcg Ser	1096
aag Lys 300	cct Pro	cag Gln	Gly 999	gag Glu	gtc Val 305	cgt Arg	gtc Val	cgt Arg	cta Leu	aag Lys 310	ggc	ggc Gly	gcc Ala	cac His	cct Pro 315	1144
gga Gly	gag Glu	ggc Gly	cgg Arg	gta Val 320	gaa Glu	gtc Val	ctg Leu	aag Lys	gcc Ala 325	agc Ser	aca Thr	tgg Trp	ggc Gly	aca Thr 330	gtc Val	1192
tgt Cys	tac Tyr	cgc Arg	aag Lys 335	tgg Trp	gac Asp	ctg Leu	cat His	gca Ala 340	gcc Ala	agc Ser	gtg Val	gtg Val	tgt Cys 345	cgg Arg	gag Glu	1240
ctg Leu	ggc Gly	ttc Phe 350	Gly	agt Ser	gct Ala	cga Arg	gaa Glu 355	gct Ala	ctg Leu	agt Ser	ggc Gly	gct Ala 360	cgc Arg	atg Met	Gly 999	1288
cag Gln	ggc Gly 365	Met	ggt Gly	gct Ala	atc Ile	cac His 370	Leu	agt Ser	gaa Glu	gtt Val	cgc Arg 375	Cys	tct Ser	gga Gly	cag Gln	1336
gag Glu 380	Leu	tcc Ser	ctc Leu	tgg Trp	aag Lys 385	Cys	ecc Pro	cac His	aag Lys	aac Asn 390	Ile	aca Thr	gct Ala	gag Glu	gat Asp 395	1384
tgt Cys	tca Ser	cat His	agc Ser	cag Gln 400	Asp	gcc Ala	ggg Gly	g gtc Val	cgg Arg 405	Cys	aac Asn	cta Leu	cct Pro	tac Tyr 410	act Thr	1432
ggg	gca Ala	gag Glu	acc Thr 415	Arg	gtc Val	ato Ile	cat His	tct Ser 420	· Val	tca Ser	cta Lev	cag Glr	ato 1 Ile 425	e Arg	a ctc g Leu	1480
agt Ser	ggg Gly	ggc Gl _y 430	/ Arc	: ago g Ser	caa Glr	cat His	gag Glu 435	ı Gly	g cga Arg	gto y Val	gaç Glı	g gtg Val 440	. Glr	ata n Ile	a ggg e Gly	1528
Gl)	cct Pro	Gl>	g ccc / Pro	ctt Leu	cgo Arg	tgg Trp 450	o Gly	c cto y Leu	ato Ile	tgt Cys	ggg Gl ₃ 455	/ Asr	gad Asp	tgg Tr	o Gly a aaa	1576
aco Thi 460	Let	g gag ı Glı	g gco ı Ala	c ato a Met	g gtg Val	L Ala	c tgt a Cys	t agg	g caa g Glr	a cto n Lei 470	ı Gly	cto Lei	g ggo ı Gly	tao Ty:	c gcc r Ala 475	1624

aac Asn	cac His	ggc Gly	ctg Leu	cag Gln 480	gag Glu	acc Thr	tgg Trp	tac Tyr	tgg Trp 485	gac Asp	tct Ser	gly ggg	aat Asn	ata Ile 490	aca Thr	1672
gag Glu	gtg Val	gtg Val	atg Met 495	agt Ser	gga Gly	gtg Val	cgc Arg	tgc Cys 500	aca Thr	gly ggg	act Thr	gag Glu	ctg Leu 505	tcc Ser	ctg Leu	1720
gat Asp	cag Gln	tgt Cys 510	gcc Ala	cat His	cat His	ggc Gly	acc Thr 515	cac His	atc Ile	acc Thr	tgc Cys	aag Lys 520	agg Arg	aca Thr	gly ggg	1768
acc Thr	cgc Arg 525	ttc Phe	act Thr	gct Ala	gga Gly	gtc Val 530	atc Ile	tgt Cys	tct Ser	gag Glu	gca Ala 535	tca Ser	gat Asp	ctg Leu	ttg Leu	1816
ctg Leu 540	cac His	tca Ser	gca Ala	ctg Leu	gtg Val 545	cag Gln	gag Glu	acc Thr	gcc Ala	tac Tyr 550	atc Ile	gaa Glu	gac Asp	cgg Arg	ccc Pro 555	1864
ctg Leu	cat His	atg Met	ttg Leu	tac Tyr 560	tgt Cys	gct Ala	gcg Ala	gaa Glu	gag Glu 565	aac Asn	tgc Cys	ctg Leu	gcc Ala	agc Ser 570	tca Ser	1912
gcc Ala	cgc Arg	tca Ser	gcc Ala 575	aac Asn	tgg Trp	ccc Pro	tat Tyr	ggt Gly 580	cac His	cgg Arg	cgt Arg	ctg Leu	ctc Leu 585	cga Arg	ttc Phe	1960
tgc Cys	tcc Ser	cag Gln 590	atc Ile	cac His	aac Asn	ctg Leu	gga Gly 595	cga Arg	gct Ala	gac Asp	ttc Phe	agg Arg 600	ccc Pro	aag Lys	gct Ala	2008
Gly 999	cgc Arg 605	cac His	tcc Ser	tgg Trp	gtg Val	tgg Trp 610	cac His	gag Glu	tgc Cys	cat His	999 Gly 615	cat His	tac Tyr	cac His	agc Ser	2056
acg Thr 620	gac Asp	ttc Phe	ttc Phe	act Thr	cac His 625	tat Tyr	gat Asp	atc Ile	ctc Leu	acc Thr 630	cca Pro	nat Xaa	ggc	acc Thr	aag Lys 635	2104
gtg Val	gct Ala	gag Glu	ggc Gly	cac His 640	Lys	gct Ala	agt Ser	ttc Phe	tgt Cys 645	ctc Leu	gaa Glu	gac Asp	act Thr	gag Glu 650	Cys	2152
cag Gln	gag Glu	gat Asp	gtc Val 655	Ser	aag Lys	cgg Arg	tat Tyr	gag Glu 660	Cys	gcc Ala	aac Asn	ttt Phe	gga Gly 665	Glu	caa Gln	2200
ggc	atc Ile	act Thr 670	Val	ggd Xaa	tgc Cys	tgg Trp	gat Asp 675	Leu	tac Tyr	cgg Arg	cat His	gac Asp 680	Ile	gac Asp	tgt Cys	2248
cag Gln	tgg Trp 685	Ile	gac Asp	ato Ile	acg Thr	gat Asp 690	Val	aag Lys	cca Pro	gga Gly	aac Asn 695	Tyr	att Ile	cto Leu	cag Gln	2296
gtt Val 700	. Val	atc Ile	aac Asn	cca Pro	aac Asn 705	Phe	gaa Glu	gta Val	gca Ala	gag Glu 710	Xaa	gac Asp	ttt Phe	acc Thr	aac Asn 715	2344
aat Asr	gca Ala	at <u>c</u> Met	aaa Lys	tgt Cys 720	Asn	tgc Cys	aaa Lys	tat Tyr	gat Asp 725	Gly	cat His	aga Arg	ato J Ile	tgg Trp 730	g gtg Val	2392

<210> 13

<211> 732

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

 $\langle 223 \rangle$ n = a or c or g or t

<400> 13

Met Arg Pro Val Ser Val Trp Gln Trp Ser Pro Trp Gly Leu Leu 1 10 15

Cys Leu Leu Cys Ser Ser Cys Leu Gly Ser Pro Ser Pro Ser Thr Gly

Pro Glu Lys Lys Ala Gly Ser Gln Gly Leu Arg Phe Arg Leu Ala Gly
35 40 45

Phe Pro Arg Lys Pro Tyr Glu Gly Arg Val Glu Ile Gln Arg Ala Gly 50 55 60

Glu Trp Gly Thr Ile Cys Asp Asp Phe Thr Leu Gln Ala Ala His 65 · 70 75 80

Ile Leu Cys Arg Glu Leu Gly Phe Thr Glu Ala Thr Gly Trp Thr His 85 90 95

Ser Ala Lys Tyr Gly Pro Gly Thr Gly Arg Ile Trp Leu Asp Asn Leu 100 105 110

Ser Cys Ser Gly Thr Glu Gln Ser Val Thr Glu Cys Ala Ser Arg Gly 115 120 125

Trp Gly Asn Ser Asp Cys Thr His Asp Glu Asp Ala Gly Val Ile Cys 130 135 140

Lys Asp Gln Arg Leu Pro Gly Phe Ser Asp Ser Asn Val Ile Glu Val 145 150 155 160

Glu His His Leu Gln Val Glu Glu Val Arg Ile Arg Pro Ala Val Gly
165 170 175

Trp Gly Arg Arg Pro Leu Pro Val Thr Glu Gly Leu Val Glu Val Arg

Leu Pro Asp Gly Trp Ser Gln Val Cys Asp Lys Gly Trp Ser Ala His
195 200 205

Asn Ser His Val Val Cys Gly Met Leu Gly Phe Pro Ser Glu Lys Arg 210 215 220

Val Asn Ala Ala Phe Tyr Arg Leu Leu Ala Gln Arg Gln Gln His Ser 225 230 235 240

Phe Gly Leu His Gly Val Ala Cys Val Gly Thr Glu Ala His Leu Ser 245 250 255

Leu Cys Ser Leu Glu Phe Tyr Arg Ala Asn Asp Thr Ala Arg Cys Pro
260 265 270

Gly Gly Pro Ala Val Val Ser Cys Val Pro Gly Pro Val Tyr Ala 275 280 285

Ala Ser Ser Gly Gln Lys Lys Gln Gln Gln Ser Lys Pro Gln Gly Glu 290 295 300

Val Arg Val Arg Leu Lys Gly Gly Ala His Pro Gly Glu Gly Arg Val 305 310 315 320

Glu Val Leu Lys Ala Ser Thr Trp Gly Thr Val Cys Tyr Arg Lys Trp \$325\$ \$330 \$35

Asp Leu His Ala Ala Ser Val Val Cys Arg Glu Leu Gly Phe Gly Ser 340 345 350

Ala Arg Glu Ala Leu Ser Gly Ala Arg Met Gly Gln Gly Met Gly Ala 355 360 365

Ile His Leu Ser Glu Val Arg Cys Ser Gly Gln Glu Leu Ser Leu Trp 370 375 380

Lys Cys Pro His Lys Asn Ile Thr Ala Glu Asp Cys Ser His Ser Gln 395 400

Asp Ala Gly Val Arg Cys Asn Leu Pro Tyr Thr Gly Ala Glu Thr Arg
405 410 415

Val Ile His Ser Val Ser Leu Gln Ile Arg Leu Ser Gly Gly Arg Ser 420 425 430

Gln His Glu Gly Arg Val Glu Val Gln Ile Gly Gly Pro Gly Pro Leu 435 440 445

- Arg Trp Gly Leu Ile Cys Gly Asp Asp Trp Gly Thr Leu Glu Ala Met 450 455 460
- Val Ala Cys Arg Gln Leu Gly Leu Gly Tyr Ala Asn His Gly Leu Gln 470 475 480
- Glu Thr Trp Tyr Trp Asp Ser Gly Asn Ile Thr Glu Val Val Met Ser 485 490 495
- Gly Val Arg Cys Thr Gly Thr Glu Leu Ser Leu Asp Gln Cys Ala His 500 505 510
- His Gly Thr His Ile Thr Cys Lys Arg Thr Gly Thr Arg Phe Thr Ala 515 520 525
- Gly Val Ile Cys Ser Glu Ala Ser Asp Leu Leu Leu His Ser Ala Leu 530 535 540
- Val Gln Glu Thr Ala Tyr Ile Glu Asp Arg Pro Leu His Met Leu Tyr 545 550 560
- Cys Ala Ala Glu Glu Asn Cys Leu Ala Ser Ser Ala Arg Ser Ala Asn 565 570 575
- Trp Pro Tyr Gly His Arg Arg Leu Leu Arg Phe Cys Ser Gln Ile His 580 585 590
- Asn Leu Gly Arg Ala Asp Phe Arg Pro Lys Ala Gly Arg His Ser Trp 595 600 605
- Val Trp His Glu Cys His Gly His Tyr His Ser Thr Asp Phe Phe Thr 610 615 620
- His Tyr Asp Ile Leu Thr Pro Xaa Gly Thr Lys Val Ala Glu Gly His 625 630 635 640
- Lys Ala Ser Phe Cys Leu Glu Asp Thr Glu Cys Gln Glu Asp Val Ser 645 650 655
- Lys Arg Tyr Glu Cys Ala Asn Phe Gly Glu Gln Gly Ile Thr Val Xaa 660 665 670
- Cys Trp Asp Leu Tyr Arg His Asp Ile Asp Cys Gln Trp Ile Asp Ile 675 680 685
- Thr Asp Val Lys Pro Gly Asn Tyr Ile Leu Gln Val Val Ile Asn Pro 690 695 700

	Manny.
	Theorem.
	Alazed
Ĺ,	Atten-
the property than	120000
1	Street,
ij.	deres.
# F	ş
-	3
22	
22	
22	
	the st. Planet
	condition of the standard
	condition of the standard
	Manage conds dgt at 18 18 Manage

Asn Phe Glu Val Ala Glu Xaa Asp Phe Thr Asn Asn Ala Met Lys Cys 705 710 715 720	
Asn Cys Lys Tyr Asp Gly His Arg Ile Trp Val His 725 730	
<210> 14 <211> 2066 <212> DNA <213> Homo sapiens	
<220> <221> CDS <222> (149)(2065)	
<400> 14 cacacgggcg cetegetege geteacacae getetgeete eteteteeeg caegegegea	60
teestecase ttccasates tgstccaggs aggagaaggs tgastggstg gastsattga	120
gctgaagaat ttccagtgac atttgtaa atg acg ccg ctc gat tcc agg ctc Met Thr Pro Leu Asp Ser Arg Leu 1 5	172
caa gcg gcc cct gcc gcc gcc gcc gcc ggg ccg aag gtg ccg ccg Gln Ala Ala Pro Ala Ala Ala Ala Ala Gly Pro Lys Val Pro Pro 10 15 20	220
agc agt ctc cag cgc agg ctt cct tac cgg gcg acc aca atg tcc gag Ser Ser Leu Gln Arg Arg Leu Pro Tyr Arg Ala Thr Thr Met Ser Glu 25 30 35 40	268
ttt ctc ctc gcc tta ctc act ctc tcg gga tta ttg ccg att gcc agg Phe Leu Leu Ala Leu Leu Thr Leu Ser Gly Leu Leu Pro Ile Ala Arg 45 50. 55	316
gtg ctg acc gtg gga gcc gac cga gat cag cag ttg tgt gat cct ggt Val Leu Thr Val Gly Ala Asp Arg Asp Gln Gln Leu Cys Asp Pro Gly 60 65 70	364
gaa ttt ctt tgc cac gat cac gtg act tgt gtc tcc cag agc tgg ctg Glu Phe Leu Cys His Asp His Val Thr Cys Val Ser Gln Ser Trp Leu 75 80 85	412
tgt gat ggg gac cct gac tgc cct gat gat tca gac gag tct tta gat Cys Asp Gly Asp Pro Asp Cys Pro Asp Asp Ser Asp Glu Ser Leu Asp 90 95 100	460
acc tgt ccc gag gag gta gaa atc aag tgc ccc ttg aat cac att gct Thr Cys Pro Glu Glu Val Glu Ile Lys Cys Pro Leu Asn His Ile Ala 105 110 115 120	508
tgc ctt ggc acc aac aaa tgt gtt cat tta tcc cag ctg tgc aat ggt Cys Leu Gly Thr Asn Lys Cys Val His Leu Ser Gln Leu Cys Asn Gly 125 130 135	556
gtc ttg gac tgc cca gat ggg tat gac gaa gga gta cat tgt cag gaa Val Leu Asp Cys Pro Asp Gly Tyr Asp Glu Gly Val His Cys Gln Glu 140 145 150	604

ctg tta tcc aat tgc caa cag ctg aat tgt cag tat aaa tgt aca atg 652

	Leu	Leu	Ser 155	Asn	Cys	Gln	Gln	Leu 160	Asn	Cys	Gln	Tyr	Lys 165	Cys	Thr	Met	
	gtc Val	aga Arg 170	aat Asn	agt Ser	aca Thr	aga Arg	tgt Cys 175	tac Tyr	tgt Cys	gag Glu	gat Asp	gga Gly 180	ttc Phe	gaa Glu	ata Ile	aca Thr	700
	gaa Glu 185	gat Asp	ggg Gly	aga Arg	agc Ser	tgt Cys 190	aaa Lys	gat Asp	caa Gln	gat Asp	gaa Glu 195	tgt Cys	gct Ala	gtt Val	tat Tyr	ggt Gly 200	748
	aca Thr	ggc Gly	agc Ser	cag Gln	acc Thr 205	tgc Cys	aga Arg	aac Asn	aca Thr	cat His 210	gga Gly	tcc Ser	tac Tyr	act Thr	tgc Cys 215	agt Ser	796
	tgt Cys	gtg Val	gaa Glu	ggc Gly 220	tac Tyr	cta Leu	atg Met	cag Gln	cca Pro 225	gac Asp	agc Ser	aga Arg	tct Ser	tgc Cys 230	aag Lys	gct Ala	844
Office St.	aaa Lys	att Ile	gaa Glu 235	cct Pro	aca Thr	gat Asp	aga Arg	cca Pro 240	cgt Arg	ata Ile	cta Leu	tta Leu	att Ile 245	gca Ala	aat Asn	ttt Phe	892
	gaa Glu	tca Ser 250	att Ile	gag Glu	gtt Val	ttc Phe	tat Tyr 255	ctt Leu	aat Asn	gga Gly	agt Ser	aaa Lys 260	att Ile	gca Ala	act Thr	cta Leu	940
hand they freely thens	agc Ser 265	tca Ser	gtc Val	aat Asn	gga Gly	aat Asn 270	gaa Glu	att Ile	cat His	act Thr	ctg Leu 275	gat Asp	ttt Phe	att Ile	tat Tyr	aat Asn 280	988
3 3 3 3 3 3 3 3	gaa Glu	gat Asp	gtg Val	att Ile	tgt Cys 285	tgg Trp	att Ile	gaa Glu	tca Ser	aga Arg 290	gaa Glu	tct [.] Ser	tca Ser	aat Asn	caa Gln 295	ctc Leu	1036
	aaa Lys	tgt Cys	atc Ile	cag Gln 300	ata Ile	aca Thr	aaa Lys	gca Ala	gga Gly 305	gga Gly	tta Leu	aca Thr	gat Asp	gaa Glu 310	tgg Trp	aca Thr	1084
entry to	atc Ile	aat Asn	att Ile 315	ctt Leu	caa Gln	tcc Ser	ttc Phe	cac His 320	aat Asn	gtg Val	caa Gln	caa Gln	atg Met 325	gcg Ala	att Ile	gac Asp	1132
	tgg Trp	ctc Leu 330	act Thr	cga Arg	aat Asn	ctc Leu	tat Tyr 335	ttt Phe	gtg Val	gac Asp	cat His	gtc Val 340	ggt Gly	gac Asp	cgg Arg	atc Ile	1180
	ttt Phe 345	gtt Val	tgt Cys	aat Asn	tcc Ser	aac Asn 350	ggt Gly	tct Ser	gta Val	tgt Cys	gtc Val 355	acc Thr	ctg Leu	att Ile	gat Asp	ctg Leu 360	1228
	gag Glu	ctt Leu	cac His	aat Asn	cct Pro 365	aaa Lys	gca Ala	ata Ile	gca Ala	gta Val 370	gat Asp	cca Pro	ata Ile	gca Ala	gga Gly 375	aaa Lys	1276
	ctt Leu	ttc Phe	ttt Phe	act Thr 380	gac Asp	tac Tyr	Gly 999	aat Asn	gtc Val 385	gcc Ala	aaa Lys	gtg Val	gag Glu	aga Arg 390	tgt Cys	gac Asp	1324
	atg Met	gat Asp	ggg 395	atg Met	aac Asn	cga Arg	aca Thr	agg Arg 400	ata Ile	att Ile	gat Asp	tca Ser	aag Lys 405	aca Thr	gag Glu	cag Gln	1372

	cca Pro	gct Ala 410	gca Ala	ctg Leu	gca Ala	cta Leu	gac Asp 415	cta Leu	gtc Val	aac Asn	aaa Lys	ttg Leu 420	gtt Val	tac Tyr	tgg Trp	gta Val	1	420
	gat Asp 425	ctt Leu	tac Tyr	ttg Leu	gac Asp	tat Tyr 430	gtg Val	gga Gly	gta Val	gtg Val	gac Asp 435	tat Tyr	caa Gln	gga Gly	aaa Lys	aat Asn 440	1	468
	aga Arg	cac His	act Thr	gtc Val	att Ile 445	caa Gln	ggc Gly	aga Arg	caa Gln	gtc Val 450	aga Arg	cat His	ctt Leu	tat Tyr	ggt Cly 455	ata Ile	1	516
	act Thr	gtg Val	ttt Phe	gaa Glu 460	gat Asp	tat Tyr	ttg Leu	tat Tyr	gca Ala 465	acc Thr	aat Asn	tct Ser	gat Asp	aac Asn 470	tac Tyr	aat Asn	1	564
	atc Ile	gta Val	agg Arg 475	ata Ile	aac Asn	cga Arg	ttt Phe	aat Asn 480	gly aaa	act Thr	gat Asp	att Ile	cac His 485	tca Ser	tta Leu	att Ile	1	612
	aaa Lys	att Ile 490	gag Glu	aat Asn	gct Ala	tgg Trp	gga Gly 495	atc Ile	cga Arg	att Ile	tat Tyr	caa Gln 500	aaa Lys	aga Arg	act Thr	caa Gln	16	660
	cca Pro 505	aca Thr	gtc Val	aga Arg	agc Ser	cat His 510	gca Ala	tgt Cys	gaa Glu	gtc Val	gat Asp 515	cca Pro	tat Tyr	gga Gly	atg Met	cca Pro 520	1'	708
Anna Cana Cana Cana Cana Cana Cana Cana	Gly aaa	ggc Gly	tgt Cys	tca Ser	cac His 525	atc Ile	tgt Cys	cta Leu	ctc Leu	agc Ser 530	agc Ser	agt Ser	tac Tyr	aaa Lys	act Thr 535	cgg Arg	1	756
25 45 25 45 26 45	act Thr	tgt Cys	cgc Arg	tgc Cys 540	agg Arg	act Thr	ggc Gly	ttc Phe	aac Asn 545	ttg Leu	gga Gly	agt Ser	gat Asp	ggc Gly 550	agg Arg	tca Ser	18	804
ATTO D	tgc Cys	aaa Lys	aga Arg 555	cca Pro	aag Lys	aat Asn	gag Glu	ttg Leu 560	ttc Phe	ctc Leu	ttt Phe	tat Tyr	999 Gly 565	aaa Lys	gga Gly	cgc Arg	18	352
	cca Pro	gga Gly 570	att Ile	gtt Val	aga Arg	gga Gly	atg Met 575	gac Asp	ttg Leu	aat Asn	acc Thr	aag Lys 580	ata Ile	gct Ala	gat Asp	gaa Glu	19	900
	Tyr 585	Met	Ile	Pro	Ile	gaa Glu 590	Asn	Leu	Val	Asn	Pro 595	Arg	Ala	Leu	Asp	Phe 600	19	948
	His	Ala	Glu	Thr	Asn 605	tac Tyr	Ile	Tyr	Phe	Ala 610	Asp	Thr	Thr	Ser	Phe 615	Leu	19	996
	att Ile	ggc Gly	cgg Arg	cag Gln 620	aag Lys	ata Ile	gat Asp	ggc Gly	aca Thr 625	gag Glu	aga Arg	gaa Glu	acc Thr	atc Ile 630	ctg Leu	aaa Lys	20	44
	gat Asp	gat Asp	ctg Leu 635	gat Asp	aat Asn	gta Val	gag Glu	g									20)66

<210> 15 <211> 639 <212> PRT

<213> Homo sapiens

<400> 15

Met Thr Pro Leu Asp Ser Arg Leu Gln Ala Ala Pro Ala Ala Ala Ala 1 5 10 15

Ala Ala Gly Pro Lys Val Pro Pro Ser Ser Leu Gln Arg Arg Leu Pro
20 25 30

Tyr Arg Ala Thr Thr Met Ser Glu Phe Leu Leu Ala Leu Leu Thr Leu 35 40 45

Ser Gly Leu Leu Pro Ile Ala Arg Val Leu Thr Val Gly Ala Asp Arg 50 55 60

Asp Gln Gln Leu Cys Asp Pro Gly Glu Phe Leu Cys His Asp His Val 65 70 75 80

Thr Cys Val Ser Gln Ser Trp Leu Cys Asp Gly Asp Pro Asp Cys Pro 85 90 95

Asp Asp Ser Asp Glu Ser Leu Asp Thr Cys Pro Glu Glu Val Glu Ile
100 105 110

Lys Cys Pro Leu Asn His Ile Ala Cys Leu Gly Thr Asn Lys Cys Val

His Leu Ser Gln Leu Cys Asn Gly Val Leu Asp Cys Pro Asp Gly Tyr 130 135 140

Asp Glu Gly Val His Cys Gln Glu Leu Leu Ser Asn Cys Gln Gln Leu 145 150 155 160

Asn Cys Gln Tyr Lys Cys Thr Met Val Arg Asn Ser Thr Arg Cys Tyr
165 170 175

Cys Glu Asp Gly Phe Glu Ile Thr Glu Asp Gly Arg Ser Cys Lys Asp 180 185 190

Gln Asp Glu Cys Ala Val Tyr Gly Thr Gly Ser Gln Thr Cys Arg Asn 195 200 205

Thr His Gly Ser Tyr Thr Cys Ser Cys Val Glu Gly Tyr Leu Met Gln 210 215 220

Pro Asp Ser Arg Ser Cys Lys Ala Lys Ile Glu Pro Thr Asp Arg Pro 225 230 235 240

- Arg Ile Leu Leu Ile Ala Asn Phe Glu Ser Ile Glu Val Phe Tyr Leu 245 250 255
- Asn Gly Ser Lys Ile Ala Thr Leu Ser Ser Val Asn Gly Asn Glu Ile $260 \\ \hspace{1.5cm} 265 \\ \hspace{1.5cm} 270 \\ \hspace{1.5cm}$
- His Thr Leu Asp Phe Ile Tyr Asn Glu Asp Val Ile Cys Trp Ile Glu 275 280 285
- Ser Arg Glu Ser Ser Asn Gln Leu Lys Cys Ile Gln Ile Thr Lys Ala 290 295 300
- Gly Gly Leu Thr Asp Glu Trp Thr Ile Asn Ile Leu Gln Ser Phe His 305 310 315
- Asn Val Gln Gln Met Ala Ile Asp Trp Leu Thr Arg Asn Leu Tyr Phe 325 330 335
- Val Asp His Val Gly Asp Arg Ile Phe Val Cys Asn Ser Asn Gly Ser 340 345 350
- Val Cys Val Thr Leu Ile Asp Leu Glu Leu His Asn Pro Lys Ala Ile 355 360 365
- Ala Val Asp Pro Ile Ala Gly Lys Leu Phe Phe Thr Asp Tyr Gly Asn 370 375 380
- Val Ala Lys Val Glu Arg Cys Asp Met Asp Gly Met Asn Arg Thr Arg 385 390 395 400
- Ile Ile Asp Ser Lys Thr Glu Gln Pro Ala Ala Leu Ala Leu Asp Leu 405 410 415
- Val Asn Lys Leu Val Tyr Trp Val Asp Leu Tyr Leu Asp Tyr Val Gly 420 425 430
- Val Val Asp Tyr Gln Gly Lys Asn Arg His Thr Val Ile Gln Gly Arg 435 440 445
- Gln Val Arg His Leu Tyr Gly Ile Thr Val Phe Glu Asp Tyr Leu Tyr 450 455 460
- Ala Thr Asn Ser Asp Asn Tyr Asn Ile Val Arg Ile Asn Arg Phe Asn 465 470 475 480
- Gly Thr Asp Ile His Ser Leu Ile Lys Ile Glu Asn Ala Trp Gly Ile 485 490 495

Arg Ile Tyr Gln Lys Arg Thr Gln Pro Thr Val Arg Ser His Ala Cys 500 Glu Val Asp Pro Tyr Gly Met Pro Gly Gly Cys Ser His Ile Cys Leu Leu Ser Ser Ser Tyr Lys Thr Arg Thr Cys Arg Cys Arg Thr Gly Phe Asn Leu Gly Ser Asp Gly Arg Ser Cys Lys Arg Pro Lys Asn Glu Leu Phe Leu Phe Tyr Gly Lys Gly Arg Pro Gly Ile Val Arg Gly Met Asp Leu Asn Thr Lys Ile Ala Asp Glu Tyr Met Ile Pro Ile Glu Asn Leu Val Asn Pro Arg Ala Leu Asp Phe His Ala Glu Thr Asn Tyr Ile Tyr Phe Ala Asp Thr Thr Ser Phe Leu Ile Gly Arg Gln Lys Ile Asp Gly 615 Thr Glu Arg Glu Thr Ile Leu Lys Asp Asp Leu Asp Asn Val Glu <210> 16 <211> 1333 <212> DNA <213> Homo sapiens <220> <221> CDS (280)..(1323) <222> <400> 16 gagatccaca cagctcggac cqqctqqatc ttqctcaqtc tctqtcaqaq qaaqatccct 60 tggaggaggc cccgcagcga catggaggga gctgctttgc tgaaagtctt tgtcctctgc 120 atctggaacc aaaatcactt cccggaattg accaactggt agactcgcct agaggggaag 180 cattgtgtcc tagttgaggc taacagtcag tatccagcct caacattcag cagaggcccc 240 agatcagcgt ctgagccagg ccaacaatga ccaaggagg atg gga tcc tgg gtg 294 Met Gly Ser Trp Val cag ctc atc aca agc gtc ggg gtg cag caa aac cat cca ggc tgg aca 342 Gln Leu Ile Thr Ser Val Gly Val Gln Gln Asn His Pro Gly Trp Thr 10 15

gtg gct gga cag ttc caa gaa aag aaa cgc ttc act gaa gaa gtc att

390

		- 33 -		
			ac ctg ggc aag go sn Leu Gly Lys Al 290	
		ı Asp Val Val As	ac ctt gtg caa ga sn Leu Val Gln As 305	
		a Lys Ser Glu Se	ct gct gag tcg ct er Ala Glu Ser Le 20	
			at gag ctc acc ca sn Glu Leu Thr Hi 34	s Ile
	cta aaa gca ggo Leu Lys Ala Gly 345		,	1333
<210> 17 <211> 348 <212> PRT <213> Homo	sapiens			
<400> 17				
Met Gly Ser	Trp Val Gln Let 5	ı Ile Thr Ser Va 10	al Gly Val Gln Gl 15	
His Pro Gly	Trp Thr Val Ala	a Gly Gln Phe Gl 25	ln Glu Lys Lys Ar 30	g Phe
Thr Glu Glu 35	Val Ile Glu Tyn	Phe Gln Lys Ly 40	ys Val Ser Pro Va 45	al His
Leu Lys Ile 50	Leu Leu Thr Sen	Asp Glu Ala Ti	rp Lys Arg Phe Va 60	al Arg
Val Ala Glu 65	Leu Pro Arg Glu 70	ı Glu Ala Asp Al 75	la Leu Tyr Glu Al 5	.a Leu 80
Lys Asn Leu	Thr Pro Tyr Val	l Ala Ile Glu As 90	sp Lys Asp Met Gl 95	

Lys Glu Gln Gln Phe Arg Glu Trp Phe Leu Lys Glu Phe Pro Gln Ile

Arg Trp Lys Ile Gln Glu Ser Ile Glu Arg Leu Arg Val Ile Ala Asn

Glu Ile Glu Lys Val His Arg Gly Cys Val Ile Ala Asn Val Val Ser

Gly Ser Thr Gly Ile Leu Ser Val Ile Gly Val Met Leu Ala Pro Phe 145 150 155 160

Thr Ala Gly Leu Ser Leu Ser Ile Thr Ala Ala Gly Val Gly Leu Gly 165 170 175

Ile Ala Ser Ala Thr Ala Gly Ile Ala Ser Ser Ile Val Glu As
n Thr 180 \$185\$ 190

Tyr Thr Arg Ser Ala Glu Leu Thr Ala Ser Arg Leu Thr Ala Thr Ser 195 200 205

Thr Asp Gln Leu Glu Ala Leu Arg Asp Ile Leu Arg Asp Ile Thr Pro 210 215 220

Asn Val Leu Ser Phe Ala Leu Asp Phe Asp Glu Ala Thr Lys Met Ile 225 230235235

Ala Asn Asp Val His Thr Leu Arg Arg Ser Lys Ala Thr Val Gly Arg 245 250 255

Pro Leu Ile Ala Trp Arg Tyr Val Pro Ile Asn Val Val Glu Thr Leu 260 270

Arg Thr Arg Gly Ala Pro Thr Arg Ile Val Arg Lys Val Ala Arg Asn 275 280 285

Leu Gly Lys Ala Thr Ser Gly Val Leu Val Val Leu Asp Val Val Asn 290 295 300

Leu Val Gln Asp Ser Leu Asp Leu His Lys Gly Ala Lys Ser Glu Ser 305 310 315 320

Ala Glu Ser Leu Arg Gln Trp Ala Gln Glu Leu Glu Glu Asn Leu Asn 325 330 335

Glu Leu Thr His Ile His Gln Ser Leu Lys Ala Gly

<210> 18

<211> 1490

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (151)..(1170)

<400> 18

agcaaaagag aaaaggagcc aggctgggct tcstgatccc acagcatcgc agagctcggg

aggcacaget cacagacaca ggaaacacag gactgetatt etgeteteet geccaeggtg													
atctggtgcc agctggtgga acagtgggtg atg gcg tcc ctg ctg caa gac cag Met Ala Ser Leu Leu Gln Asp Gln 1 5													
ctg acc act gat cag g Leu Thr Thr Asp Gln A 10													
cgc aag gtg agg tcc a Arg Lys Val Arg Ser I 25:													
cag aat gac ggc atg a Gln Asn Asp Gly Met 7 45													
gcc aag ccc agc ttc t Ala Lys Pro Ser Phe S 60													
cat gat tcc gag ttg c His Asp Ser Glu Leu I 75													
cag ggc ttc acc att g Gln Gly Phe Thr Ile \ . 90													
atg gcc aac agt gtt c Met Ala Asn Ser Val C 105		22 2 2											
ctg ttg gtg gat ctt g Leu Leu Val Asp Leu V 125													
caa tgg ctg agc gat t Gln Trp Leu Ser Asp T 140		Gly Asp Lys Asn											
aag atg agt ttc caa g Lys Met Ser Phe Gln G 155	Glu Val Gln Arg	-											
gaa atg gac caa gaa t Glu Met Asp Gln Glu 7 170													
tcc cag tct gga acc c Ser Gln Ser Gly Thr I 185													
gca ttg act aaa cgt g Ala Leu Thr Lys Arg A 205													
gct gat ggg cag aag c Ala Asp Gly Gln Lys I 220		Glu Phe Leu Asp											
gag gag cag aag gag a	aga gac tgc acc	tct gag ctt gct	ctg gaa ctc 894										

(3lu	Glu	Gln 235	Lys	Glv	Arg	Asp	Cys 240	Thr	Ser	Glu	Leu	Ala 245	Leu	Glu	Leu	
-	att	gac Asp 250	cgc Arg	tat Tyr	gaa Glu	cct Pro	tca Ser 255	gac Asp	agt Ser	ggc Gly	aaa Lys	ctg Leu 260	cgg Arg	cat His	gtg Val	ctg Leu	942
Ş	agt Ser 265	atg Met	gat Asp	ggc Gly	ttc Phe	ctc Leu 270	agc Ser	tac Tyr	ctc Leu	tgc Cys	tct Ser 275	aag Lys	gat Asp	gga Gly	gac Asp	atc Ile 280	990
ţ	tc Phe	aac Asn	cca Pro	gcc Ala	tgc Cys 285	ctc Leu	ccc Pro	atc Ile	tat Tyr	cag Gln 290	gat Asp	atg Met	act Thr	caa Gln	ccc Pro 295	ctg Leu	1038
ā P	aac Asn	cac His	tac Tyr	ttc Phe 300	atc Ile	tgc Cys	tct Ser	tct Ser	cat His 305	aac Asn	acc Thr	tac Tyr	cta Leu	gtg Val 310	ggg Gly	gac Asp	1086
(cag 31n	ctt Leu	tgc Cys 315	ggc	cag Gln	agc Ser	agc Ser	gtc Val 320	gag Glu	gga Gly	tat Tyr	ata Ile	cgg Arg 325	tgc Cys	agt Ser	ggt Gly	1134
Ć	ggt 31y	aga Arg 330	gaa Glu	gly aaa	gtc Val	caa Gln	ctc Leu 335	atg Met	aga Arg	Gly 999	acc Thr	atg Met 340	taga	aaaq	gtg		1180
ā	ŧgg <u>c</u>	ggago	ctg t	cagt	gtct	a ac	cagat	tggg	g aca	agtgt	tgt	gggg	gttt	ag g	agget	gagga	1240
ć	gaad	ctgga	ata d	ccaga	agaca	ac tt	ggag	ggaga	a tat	tgaa	agac	tggt	ggga	aga a	etggt	aatga	1300
ā	acc	cctat	agg g	gtcaa	atgga	aa ct	tctc	ctttc	c aca	aagct	atg	aaac	ctctc	ect 9	ggaad	ctcaga	1360
ć	ggco	cctga	aca g	gattt	catat	it ta	acaa	aatta	a ata	aaaca	agat	tgtt	aaat	gg a	aggo	caatag	1420
ā	Igaa	atagg	gag t	taaa	aata	at ag	ggtto	etgga	a gto	cagad	ccat	ctga	aatt	at a	atcot	agctc	1480
	ttt	actt	gg														1490
<	210		19														

<211> 340

<212> PRT

<213> Homo sapiens

<400> 19

Met Ala Ser Leu Leu Gln Asp Gln Leu Thr Thr Asp Gln Asp Leu Leu

Leu Met Gln Glu Gly Met Pro Met Arg Lys Val Arg Ser Lys Ser Trp 20

Lys Lys Leu Arg Tyr Phe Arg Leu Gln Asn Asp Gly Met Thr Val Trp

His Ala Arg Gln Ala Arg Gly Ser Ala Lys Pro Ser Phe Ser Ile Ser

Asp Val Glu Thr Ile Arg Asn Gly His Asp Ser Glu Leu Leu Arg Ser 65 70 75 80

Leu Ala Glu Glu Leu Pro Leu Glu Gln Gly Phe Thr Ile Val Phe His 85 90 95

Gly Arg Arg Ser Asn Leu Asp Leu Met Ala Asn Ser Val Glu Glu Ala 100 105 110

Gln Ile Trp Met Arg Gly Leu Gln Leu Leu Val Asp Leu Val Thr Ser \$125\$

Met Asp His Gln Glu Arg Leu Asp Gln Trp Leu Ser Asp Trp Phe Gln 130 135 140

Arg Gly Asp Lys Asn Gln Asp Gly Lys Met Ser Phe Gln Glu Val Gln 145 150 155 160

Arg Leu Leu His Leu Met As
n Val Glu Met Asp Gl
n Glu Tyr Ala Phe\$165\$ \$170\$ \$175\$

Ser Leu Phe Gln Ala Ala Asp Thr Ser Gln Ser Gly Thr Leu Glu Gly
180 185 190

Glu Glu Phe Val Gln Phe Tyr Lys Ala Leu Thr Lys Arg Ala Glu Val 195 200 205

Gln Glu Leu Phe Glu Ser Phe Ser Ala Asp Gly Gln Lys Leu Thr Leu 210 215 220

Leu Glu Phe Leu Asp Phe Leu Gln Glu Glu Gln Lys Glu Arg Asp Cys 235 230 235

Thr Ser Glu Leu Ala Leu Glu Leu Ile Asp Arg Tyr Glu Pro Ser Asp \$245\$ \$250\$

Ser Gly Lys Leu Arg His Val Leu Ser Met Asp Gly Phe Leu Ser Tyr $260 \hspace{1.5cm} 265 \hspace{1.5cm} 270 \hspace{1.5cm}$

Leu Cys Ser Lys Asp Gly Asp Ile Phe Asn Pro Ala Cys Leu Pro Ile 275 280 285

Tyr Gln Asp Met Thr Gln Pro Leu Asn His Tyr Phe Ile Cys Ser Ser 290 295 300

His Asn Thr Tyr Leu Val Gly Asp Gln Leu Cys Gly Gln Ser Ser Val 305 310 315

Glu Gly Tyr Ile Arg Cys Ser Gly Gly Arg Glu Gly Val Gln Leu Met 325 330 335

Arg Gly Thr Met

340	
<210> 20 <211> 2035 <212> DNA <213> Homo sapiens	
<220> <221> CDS <222> (189)(1415)	
<400> 20 ccaactaagc ttgcctaatt tgcttcagaa ttggaagagg gaattgcagc aggaaaatat	60
gtgaagagtt tttaaaccca caaattette ttaetttaga attagttgtt acattggeag	120
gaaaaaataa atgcagatgt tggaccatgt tggaaacctt gtcaagacag tggattgtct	180
cacacaga atg gaa atg tgg ctt ctg att ctg gtg gcg tat atg ttc cag Met Glu Met Trp Leu Leu Ile Leu Val Ala Tyr Met Phe Gln 1 5 10	230
aga aat gtg aat tca gta cat atg cca act aaa gct gtg gac cca gaa Arg Asn Val Asn Ser Val His Met Pro Thr Lys Ala Val Asp Pro Glu 15 20 25 30	278
gca ttc atg aat att agt gaa atc atc caa cat caa ggc tat ccc tgt Ala Phe Met Asn Ile Ser Glu Ile Ile Gln His Gln Gly Tyr Pro Cys 35 40 45	326
gag gaa tat gaa gtc gca act gaa gat ggg tat atc ctt tct gtt aac Glu Glu Tyr Glu Val Ala Thr Glu Asp Gly Tyr Ile Leu Ser Val Asn 50 55 60	374
agg att cct cga ggc cta gtg caa cct aag aag aca ggt tcc agg cct Arg Ile Pro Arg Gly Leu Val Gln Pro Lys Lys Thr Gly Ser Arg Pro 65 70 75	422
gtg gtg tta ctg cag cat ggc cta gtt gga ggt gct agc aac tgg att Val Val Leu Leu Gln His Gly Leu Val Gly Gly Ala Ser Asn Trp Ile 80 85 90	470
tcc aac ctg ccc aac aat agc ctg ggc ttc att ctg gca gat gct ggt Ser Asn Leu Pro Asn Asn Ser Leu Gly Phe Ile Leu Ala Asp Ala Gly 95 100 105 110	518
ttt gac gtg tgg atg ggg aac agc agg gga aac gcc tgg tct cga aaa Phe Asp Val Trp Met Gly Asn Ser Arg Gly Asn Ala Trp Ser Arg Lys 115 120 125	566
cac aag aca ctc tcc ata gac caa gat gag ttc tgg gct ttc agt tat His Lys Thr Leu Ser Ile Asp Gln Asp Glu Phe Trp Ala Phe Ser Tyr 130 135 140	614
gat gag atg gct agg ttt gac ctt cct gca gtg ata aac ttt att ttg Asp Glu Met Ala Arg Phe Asp Leu Pro Ala Val Ile Asn Phe Ile Leu 145 150 155	662

						aag Lys 165										710
						gca Ala										758
						gct Ala										806
-		_				aaa Lys			-	_		_	_			854
						aaa Lys										902
						ctt Leu 245										950
_	_			_		ctt Leu									_	998
	_	_	_	_	_	gta Val		_	_				-			1046
						cac His		_	_	_					_	1094
		-		-		Gly 999	_					_	_		-	1142
	_				_	agg Arg 325		-	-	-	_	_	_	_		1190
	_	_				ggt Gly	_	_						_		1238
						gag Glu										1286
						gtg Val										1334
						atc Ile										1382
						tgt Cys 405					tga	agca	tct	gaca	ctgacg	1435

atcttaggac aacctcctga gggatggggc taggacccat gaaggcagaa ttatggagag 1495 caqaqaccta qtatacattt ttcagattcc ctgcacttgg cactaaatcc gacacttaca 1555 tttacatttt ttttctgtaa attaaagtac ttattaggta aatagaggtt ttgtatgcta 1615 ttatatattc taccatcttg aagggtaggt tttacctgat agccagaaaa tatctagaca 1675 ttototatat cattoaggta aatotottta aaacacctat tgttttttot ataagccata 1735 tttttggagc actaaagtaa aatggcaaat tgggacagat attgaggtct ggagtctgtg 1795 gattattgtt gactttgaca aaataagcta gacattttca cettgttgcc acagagacat 1855 aacactacct caggaagctg agctgcttta aggacaacaa caacaaaatc agtgttacag 1915 tatggatgaa atctatgtta agcattctca gaataaggcc aagttttata gttgcatctc 1975 agggaagaaa attttatagg atgtttatga gttctccaat aaatgcattc tgcattacat 2035

<210> 21

<211> 409

<212> PRT

<213> Homo sapiens

<400> 21

Met Glu Met Tro Leu Leu Ile Leu Val Ala Tyr Met Phe Gln Arg Asn 1 5 10 15

Val Asn Ser Val His Met Pro Thr Lys Ala Val Asp Pro Glu Ala Phe 20 25 30

Met Asn Ile Ser Glu Ile Ile Gln His Gln Gly Tyr Pro Cys Glu Glu 35 40 45

Tyr Glu Val Ala Thr Glu Asp Gly Tyr Ile Leu Ser Val Asn Arg Ile 50 55 60

Pro Arg Gly Leu Val Gln Pro Lys Lys Thr Gly Ser Arg Pro Val Val 65 70 75 80

Leu Leu Gln His Gly Leu Val Gly Gly Ala Ser Asn Trp Ile Ser Asn 85 90 95

Leu Pro Asn Asn Ser Leu Gly Phe Il'e Leu Ala Asp Ala Gly Phe Asp
100 105 110

Val Trp Met Gly Asn Ser Arg Gly Asn Ala Trp Ser Arg Lys His Lys 115 120 125

Thr Leu Ser Ile Asp Gln Asp Glu Phe Trp Ala Phe Ser Tyr Asp Glu 130 135 140

Met Ala Arg Phe Asp Leu Pro Ala Val Ile Asn Phe Ile Leu Gln Lys 145 150 150 160

Thr Gly Gln Glu Lys Ile Tyr Tyr Val Gly Tyr Ser Gln Gly Thr Thr \$165\$ \$170\$ \$175\$

Met Gly Phe Ile Ala Phe Ser Thr Met Pro Glu Leu Ala Gln Lys Ile 180 185 190

Lys Met Tyr Phe Ala Leu Ala Pro Ile Ala Thr Val Lys His Ala Lys 195 200 205

Ser Pro Gly Thr Lys Phe Leu Leu Pro Asp Met Met Ile Lys Gly 210 215 220

Leu Phe Gly Lys Lys Glu Phe Leu Tyr Gln Thr Arg Phe Leu Arg Gln 225 230 235 240

Leu Val Ile Tyr Leu Cys Gly Gln Val Ile Leu Asp Gln Ile Cys Ser 245 250 255

Asn Ile Met Leu Leu Gly Gly Phe Asn Thr Asn Asn Met Asn Met 260 265 270

Ser Arg Ala Ser Val Tyr Ala Ala His Thr Leu Ala Gly Thr Ser Val 275 280 285

Gln Asn Ile Leu His Trp Ser Gln Ala Val Asn Ser Gly Glu Leu Arg 290 295 300

Ala Phe Asp Trp Gly Ser Glu Thr Lys Asn Leu Glu Lys Cys Asn Gln 305 310 315 320

Pro Thr Pro Val Arg Tyr Arg Val Arg Asp Met Thr Val Pro Thr Ala 325 330 335

Met Trp Thr Gly Gly Gln Asp Trp Leu Ser Asn Pro Glu Asp Val Lys 340 345 350

Met Leu Leu Ser Glu Val Thr Asn Leu Ile Tyr His Lys Asn Ile Pro 355 360 365

Glu Trp Ala His Val Asp Phe Ile Trp Gly Leu Asp Ala Pro His Arg 370 380

Met Tyr Asn Glu Ile Ile His Leu Met Gln Gln Glu Glu Thr Asn Leu 385 390 395 400

Ser Gln Gly Arg Cys Glu Ala Val Leu 405

<210: <211: <212: <213:	> 2 > E	:2 :224 :NA Iomo	sapi	.ens												
<220: <221: <223:	> n	nisc_ n = a	_		go	or t										
<220: <221: <222: <223:	> (CDS (82). Kaa =			n or	othe	er									
<400 tgct		22 :ga a	ıctaç	gctca	ıc aç	gtago	ccgg	agg	jecea	ıggg	caat	ccga	acc a	catt	tcact	60
ctca	ccgo	etg t	agga	atco	ca g	_		gcc Ala	_		-	_	-			111
atg Met :																159
tct (207
ccc Pro																255
ttg Leu																303
tac Tyr 75																351
gaa Glu																399
aat Asn																447
cgt Arg		_				_		-			_	_		_		495
gaa Glu							_		_		_				_	543

agc aaa agt tgg gag gac tgt aaa tat ttc tgc ctt agt gaa aac tct Ser Lys Ser Trp Glu Asp Cys Lys Tyr Phe Cys Leu Ser Glu Asn Ser 155 160 165 170	
acc atg ctg aag ata aac aaa caa gaa gac ctg gaa ttt gcc gcg tct Thr Met Leu Lys Ile Asn Lys Gln Glu Asp Leu Glu Phe Ala Ala Ser 175 180 185	
cag agc tac tct gag ttt ttc tac tct tat tgg aca ggg ctt ttg cgc Gln Ser Tyr Ser Glu Phe Phe Tyr Ser Tyr Trp Thr Gly Leu Leu Arg	
cct gac agt ggc aag gcc tgg ctg tgg atg gat gga acc cct ttc act Pro Asp Ser Gly Lys Ala Trp Leu Trp Met Asp Gly Thr Pro Phe Thr 205 210 215	
tct gaa ctg ttc cat att ata ata gat gtc acc agc cca aga agc aga Ser Glu Leu Phe His Ile Ile Ile Asp Val Thr Ser Pro Arg Ser Arg 220 225 230	
gac tgt gtg gcc atc ctt aat ggg atg atc ttc tca aag gac tgc aaa Asp Cys Val Ala Ile Leu Asn Gly Met Ile Phe Ser Lys Asp Cys Lys 235 240 245 250	
gaa ttg aag cgt tgt gtc tgt gag aga agg gca gga atg gtg aag cca Glu Leu Lys Arg Cys Val Cys Glu Arg Arg Ala Gly Met Val Lys Pro 255 260 265	
gag agc ctc cat gtc ccc cct gaa aca tta ggc gaa ggt gac Glu Ser Leu His Val Pro Pro Glu Thr Leu Gly Glu Gly Asp 270 275 280	921
tgattcgccc tctgcaacta caaatagcag agtgagccag gcggtgccaa agcaaggg	jct 981
tgattcgccc tctgcaacta caaatagcag agtgagccag gcggtgccaa agcaaggg agttgagaca ttgggaaatg gaacataatc aggaaagact atctctctga ctagtaca	,
	aa 1041
agttgagaca ttgggaaatg gaacataatc aggaaagact atctctctga ctagtaca	iaa 1041 icg 1101
agttgagaca ttgggaaatg gaacataatc aggaaagact atctctctga ctagtaca atgggttctc gtgtttcctg ttcaggatca ccagcatttc tgagcttggg tttatgca	laa 1041 log 1101 laa 1161
agttgagaca ttgggaaatg gaacataatc aggaaagact atctctctga ctagtaca atgggttctc gtgtttcctg ttcaggatca ccagcatttc tgagcttggg tttatgca tatttaacag tcacaagaag tcttatttac atgccaccaa ccaacctcag aaacccat	aa 1041 acg 1101 aa 1161 aat 1221
agttgagaca ttgggaaatg gaacataatc aggaaagact atctctctga ctagtaca atgggttctc gtgtttcctg ttcaggatca ccagcatttc tgagcttggg tttatgca tatttaacag tcacaagaag tcttatttac atgccaccaa ccaacctcag aaacccat tgtcatctgc cttcttggct tagagataac ttttagctct ctttcttct aatgtcta	aa 1041 acg 1101 aa 1161 aat 1221 gta 1281
agttgagaca ttgggaaatg gaacataatc aggaaagact atctctctga ctagtaca atgggttctc gtgtttcctg ttcaggatca ccagcatttc tgagcttggg tttatgca tatttaacag tcacaagaag tcttatttac atgccaccaa ccaacctcag aaacccat tgtcatctgc cttcttggct tagagataac ttttagctct ctttcttct aatgtcta atcacctccc tgttttcatg tcttccttac acttggtgga ataagaaact ttttgaag	1041 102 1101 103 1161 104 1221 105 1281 106 1341
agttgagaca ttgggaaatg gaacataatc aggaaagact atctctctga ctagtaca atgggttctc gtgtttcctg ttcaggatca ccagcatttc tgagcttggg tttatgca tatttaacag tcacaagaag tcttatttac atgccaccaa ccaacctcag aaacccat tgtcatctgc cttcttggct tagagataac ttttagctct ctttcttctc aatgtcta atcacctccc tgttttcatg tcttccttac acttggtgga ataagaaact ttttgaag gaggaaatac attgaggtaa catccttttc tctgacagtc aagtagtcca tcagaaat	1041 102 1101 103 1161 104 1221 105 1281 107 1341 108 1401
agttgagaca ttgggaaatg gaacataatc aggaaagact atctctctga ctagtaca atgggttctc gtgtttcctg ttcaggatca ccagcatttc tgagcttggg tttatgca tatttaacag tcacaagaag tcttatttac atgccaccaa ccaacctcag aaacccat tgtcatctgc cttcttggct tagagataac ttttagctct ctttcttctc aatgtcta atcacctccc tgttttcatg tcttccttac acttggtgga ataagaaact ttttgaag gaggaaatac attgaggtaa catccttttc tctgacagtc aagtagtcca tcagaaat gcagtcactt cccagattgt accagcaaat acacaaggaa ttctttttgt ttgtttca	1041 101 101 101 101 101 101 101 101 101
agttgagaca ttgggaaatg gaacataatc aggaaagact atctctctga ctagtaca atgggttctc gtgtttcctg ttcaggatca ccagcatttc tgagcttggg tttatgca tatttaacag tcacaagaag tcttatttac atgccaccaa ccaacctcag aaacccat tgtcatctgc cttcttggct tagagataac ttttagctct ctttcttctc aatgtcta atcacctccc tgttttcatg tcttccttac acttggtgga ataagaaact ttttgaag gaggaaatac attgaggtaa catccttttc tctgacagtc aagtagtcca tcagaaat gcagtcactt cccagattgt accagcaaat acacaaggaa ttctttttgt ttgtttcat tcatactagt cccttcccaa tccatcagta aagaccccat ctgccttgtc catgccgt	1041 101 101 101 101 101 101 101 101 101
agttgagaca ttgggaaatg gaacataatc aggaaagact atctctctga ctagtaca atgggttctc gtgtttcctg ttcaggatca ccagcatttc tgagcttggg tttatgca tatttaacag tcacaagaag tcttatttac atgccaccaa ccaacctcag aaacccat tgtcatctgc cttcttggct tagagataac ttttagctct ctttcttctc aatgtcta atcacctccc tgttttcatg tcttccttac acttggtgga ataagaaact ttttgaag gaggaaatac attgaggtaa catccttttc tctgacagtc aagtagtcca tcagaaat gcagtcactt cccagattgt accagcaaat acacaaggaa ttctttttgt ttgtttcat tcatactagt cccttcccaa tccatcagta aagaccccat ctgccttgtc catgccgt cccaacaggg atgtcacttg atatgagaat ctcaaatctc aatgccttat aagcattc	1041 102 1101 103 1161 1041 1221 1041 1281 1041 1401 1041 1461 1041 1521 1041 1581
agttgagaca ttgggaaatg gaacataatc aggaaagact atctcttga ctagtaca atgggttctc gtgtttcctg ttcaggatca ccagcatttc tgagcttggg tttatgca tatttaacag tcacaagaag tcttatttac atgccaccaa ccaacctcag aaacccat tgtcatctgc cttcttggct tagagataac ttttagctct ctttcttctc aatgtcta atcacctccc tgttttcatg tcttccttac acttggtgga ataagaaact ttttgaag gaggaaatac attgaggtaa catccttttc tctgacagtc aagtagtcca tcagaaat gcagtcactt cccagattgt accagcaaat acacaaggaa ttctttttgt ttgtttcat tcatactagt cccttcccaa tccatcagta aagaccccat ctgccttgtc catgccgt cccaacaggg atgtcactt gataattgt ctcaaatctc aatgccttat aagcattc tcctgtgtcc attaagactc tgataattgt ctccctcca taggaatttc tcccagga	taa 1041 tcg 1101 taa 1161 taa 1221 gta 1281 ttg 1341 ttg 1401 ttt 1461 tct 1521 taa 1581 gag 1641
agttgagaca ttgggaaatg gaacataatc aggaaagact atctctctga ctagtaca atgggttctc gtgtttcctg ttcaggatca ccagcatttc tgagcttggg tttatgca tatttaacag tcacaagaag tcttatttac atgccaccaa ccaacctcag aaacccat tgtcatctgc cttcttggct tagagataac ttttagctct ctttcttctc aatgtcta atcacctccc tgttttcatg tcttccttac acttggtgga ataagaaact ttttgaag gaggaaatac attgaggtaa catccttttc tctgacagtc aagtagtcca tcagaaat gcagtcactt cccagattgt accagcaaat acacaaggaa ttctttttgt ttgtttcat tcatactagt cccttcccaa tccatcagta aagaccccat ctgccttgtc catgccgt cccaacaggg atgtcacttg atatgagaat ctcaaatctc aatgccttat aagcattc tcctgtgtcc attaagactc tgataattgt ctcccctcca taggaatttc tcccagga gaaatatatc cccatcccg tttcatactag gaactaccgt ccccgatatt cccttcagga gaaatatatc cccatcccg tttcatatca gaactaccgt ccccgatatt cccttcagga	1041 102 1101 103 1101 1041 1101 1041 1121 1121 1121 1121
agttgagaca ttgggaaatg gaacataatc aggaaagact atctcttga ctagtaca atgggttctc gtgtttcctg ttcaggatca ccagcatttc tgagcttggg tttatgca tatttaacag tcacaagaag tcttatttac atgccaccaa ccaacctcag aaacccat tgtcatctgc cttcttggct tagagataac ttttagctct ctttcttctc aatgtcta atcacctccc tgttttcatg tcttccttac acttggtgga ataagaaact ttttgaag gaggaaatac attgaggtaa catccttttc tctgacagtc aagtagtcca tcagaaat gcagtcactt cccagattgt accagcaaat acacaaggaa ttcttttgt ttgttcatcatactagt cccttcccaa tccatcagta aagaccccat ctgccttgtc catgccgt cccaacaggg atgtcacttg atatgagaat ctcaaatctc aatgccttat aagcattc tcctgtgtcc attaagactc tgataattgt ctcccctcca taggaatttc tcccagga gaaatatatc cccatcccg tttcatatca gaactaccgt ccccgatatt cccttcagagatagatacagagataccccat ctgccttgtc catgcagagagaatatatac cccatcccg tttcatatca gaactaccgt ccccgatatt cccttcagagatagatacagagataaaaga ccagaaaaaa gtgagcctct tcatctgcac ctgtaatagt ttcagttcag	1041 102 1101 103 1161 1041 1221 1041 1281 1041 1401 1041 1521 1041 1521 1041 1521 1041 1701 1041 1761

gtttttgggg aatttacaag agtactgatt acatgattat ctggagaaaa taagatgtct 1941
ttgaaataca tgttggcttc aagaaaacag ttttaacgtt ttcctaaaat gaaatctttt 2001
gaggtgagct tatggcatca acacatggtt gatgaggaag ctgagttgca ttagtgcaca 2061
tgatttccag tcaggtcatg ggaaatgaac agagacagtg acatctttgt agctgctcct 2121
ttgtgaggca cttctttctt gagatgactc catgcacaaa tataacaggg atcattggga 2181
atgacaccat cacagccacc aagnttattg ggttactgat aat 2224

<210> 23

<211> 280

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> n = a or c or g or t

<400> 23

Met Gln Ala Lys Tyr Ser Ser Thr Arg Asp Met Leu Asp Asp Gly 1 5 10 15

Asp Thr Thr Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr Arg His $20 \\ 25 \\ 30$

Pro Glu Pro Arg Arg Thr Glu His Arg Ala Pro Ser Ser Thr Trp Arg 35 40 45

Pro Val Ala Leu Thr Leu Leu Thr Leu Cys Leu Val Leu Leu Ile Gly 50 55 60

Leu Ala Ala Leu Gly Leu Leu Phe Phe Gln Tyr Tyr Gln Leu Ser Asn 65 70 75 80

Thr Gly Gln Asp Thr Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr 85 90 95

Ser Gln Glu Leu Gln Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly
100 105 110

Ser Leu Gln His Val Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys 115 120 125

Ala Gly Ala His Arg Cys Ser Pro Cys Thr Glu Gln Trp Lys Trp His 130 135

Gly Asp Asn Cys Tyr Gln Phe Tyr Lys Asp Ser Lys Ser Trp Glu Asp 145 150 155

Cys	Lys	Tyr	Phe	Cys 165	Leu	Ser	Glu	Asn	Ser 170	Thr	Met	Leu	Lys	Ile 175	Asn		
Lys	Gln	Glu	Asp 180	Leu	Glu	Phe	Ala	Ala 185	Ser	Gln	Ser	Tyr	Ser 190	Glu	Phe		
Phe	Tyr	Ser 195	Tyr	Trp	Thr	Gly	Leu 200	Leu	Arg	Pro	Asp	Ser 205	Gly	Lys	Ala		
Trp	Leu 210	Trp	Met	Asp	Gly	Thr 215	Pro	Phe	Thr	Ser	Glu 220	Leu	Phe	His	Ile		
Ile 225	Ile	Asp	Val	Thr	Ser 230	Pro	Arg	Ser	Arg	Asp 235	Cys	Val	Ala	Ile	Leu 240		
Asn	Gly	Met	Ile	Phe 245	Ser	Lys	Asp	Cys	Lys 250	Glu	Leu	Lys	Arg	Сув 255	Val		
Cys	Glu	Arg	Arg 260	Ala	Gly	Met	Val	Lys 265	Pro	Glu	Ser	Leu	His 270	Val	Pro		
Pro	Glu	Thr 275	Leu	Gly	Glu	Gly	Asp 280										
<210 <211 <211 <211	1> 9 2> I	24 996 DNA Homo	sapi	iens													
<220 <221 <222	1> (CDS (38)	(9	79)													
<400		24 cat t	tcad	ctcto	ca co	egetç	gtggg	g aat	ccag			_		_	c agc r Ser	55	
	acg Thr															103	
cat His	tct Ser	caa Gln 25	gcc Ala	tct Ser	gcc Ala	aca Thr	act Thr 30	cgg Arg	cat His	cca Pro	gag Glu	ccc Pro 35	cgg Arg	cgc Arg	aca Thr	151	
gag Glu	cac His 40	agg Arg	gct Ala	ccc Pro	tct Ser	tca Ser 45	acg Thr	tgg Trp	cga Arg	cca Pro	gtg Val 50	gcc Ala	ctg Leu	acc Thr	ctg Leu	199	
	act Thr															247	
ttg	ttt	ttt	cag	tac	tac	cag	ctc	tcc	aat	act	ggt	caa	gac	acc	att	295	

Leu	Phe	Phe	Gln	Tyr 75	Tyr	Gln	Leu	Ser	Asn 80	Thr	Gly	Gln	Asp	Thr 85	Ile	
tct Ser	caa Gln	atg Met	gaa Glu 90	gaa Glu	aga Arg	tta Leu	gga Gly	aat Asn 95	acg Thr	tcc Ser	caa Gln	gag Glu	ttg Leu 100	caa G]n	tct Ser	343
								gca Ala								391
								aac Asn								439
aac Asn 135	atg Met	gtg Val	cca Pro	gca Alə	tct Ser 140	gct Ala	tct Ser	tct Ser	gag Glu	agc Ser 145	ctc Leu	agg Arg	cag Gln	ctt Leu	cca Pro 150	487
								cac His								535
								tgc Cys 175								583
								ttc Phe								631
_	_	_					_	gac Asp	_	-		_				679
								tat Tyr								727
_			_	_		_		atg Met								775
								gtc Val 255								823
_		_					_				_	_	_		gaa Glu	871
															gag Glu	919
								tta Leu								967
	cat His		cat His	tag	ccta	ggt	tcta	gac								996

<210> 25

<211> 314

<212> PRT

<213> Homo sapiens

<400> 25

Met Gln Ala Lys Tyr Ser Ser Thr Met Asp Met Leu Asp Asp Gly
1 10 15

Asp Thr Thr Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr Arg His $20 \\ 25 \\ 30 \\$

Pro Glu Pro Arg Arg Thr Glu His Arg Ala Pro Ser Ser Thr Trp Arg 35 40 45

Pro Val Ala Leu Thr Leu Leu Thr Leu Cys Leu Val Leu Leu Ile Gly 50 55 60

Leu Ala Ala Leu Gly Leu Leu Phe Phe Gln Tyr Tyr Gln Leu Ser Asn 65. 70 75 80

Thr Gly Gln Asp Thr Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr 85 90 95

Ser Gln Glu Leu Gln Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly
100 105 110

Ser Leu Gln His Val Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys 115 120 125

Ala Gly Gly Tyr Thr Arg Asn Met Val Pro Ala Ser Ala Ser Ser Glu
130 135 140

Cys Ser Pro Cys Thr Glu Gln Trp Lys Trp His Gly Asp Asn Cys Tyr 165 170 175

Gln Phe Tyr Lys Asp Ser Lys Ser Trp Glu Asp Cys Lys Tyr Phe Cys
180 185 190

Leu Ser Glu Asn Ser Thr Met Leu Lys Ile Asn Lys Gln Glu Asp Leu 195 200 205

Glu Phe Ala Ala Ser Gln Ser Tyr Ser Glu Phe Phe Tyr Ser Tyr Trp 210 215 220

Thr Gly Leu Leu Arg Pro Asp Ser Gly Lys Ala Trp Leu Trp Met Asp 225 230 235 240	
Gly Thr Pro Phe Thr Ser Glu Leu Phe His Ile Ile Ile Asp Val Thr 245 250 255	
Ser Pro Arg Ser Arg Asp Cys Val Ala Ile Leu Asn Gly Met Ile Phe 260 265 270	
Ser Lys Asp Cys Lys Glu Leu Lys Arg Cys Val Cys Glu Arg Arg Ala 275 280 285	
Gly Met Val Lys Pro Glu Ser Leu His Val Pro Pro Glu Thr Leu Gly 290 295 300	
Glu Gly Asp Met His His His His His His 305 310	
<210> 26 <211> 2125 <212> DNA <213> Homo sapiens	
<220> <221> misc_feature <223> n = a or c or g or t	
<220> <221> CDS <222> (82)(822) <223> Xaa = Unknown or other	
<400> 26 tgcttcctga actagctcac agtagcccgg cggcccaggg caatccgacc acatttcact	60
ctcaccgctg taggaatcca g atg cag gcc aag tac agc agc acg agg gac Met Gln Ala Lys Tyr Ser Ser Thr Arg Asp 1 5 10	111
atg ctg gat gat gag gac acc acc atg agc ctg cat tct caa gcc Met Leu Asp Asp Asp Gly Asp Thr Thr Met Ser Leu His Ser Gln Ala 15 20 25	159
tct gcc aca act cgg cat cca gag ccc cgg cgc aca gtt ttt cag tac Ser Ala Thr Thr Arg His Pro Glu Pro Arg Arg Thr Val Phe Gln Tyr 30 35 40	207
tac cag ctc tcc aat act ggt caa gac acc att tct caa atg gaa gaa Tyr Gln Leu Ser Asn Thr Gly Gln Asp Thr Ile Ser Gln Met Glu Glu 45 50 55	255
aga tta gga aat acg tcc caa gag ttg caa tct ctt caa gtc cag aat Arg Leu Gly Asn Thr Ser Gln Glu Leu Gln Ser Leu Gln Val Gln Asn	303

ata Ile 75	aag Lys	ctt Leu	gca Ala	gga Gly	agt Ser 80	ctg Leu	cag Gln	cat His	gtg Val	gct Ala 85	gaa Glu	aaa Lys	ctc Leu	tgt Cys	cgt Arg 90	351
gag Glu	ctg Leu	tat Tyr	aac Asn	aaa Lys 95	gct Ala	gga Gly	gca Ala	cac His	agg Arg 100	tgc Cys	agc Ser	cct Pro	tgt Cys	aca Thr 105	gaa Glu	399
caa Gln	tgg Trp	aaa Lys	tgg Trp 110	cat His	gga Gly	gac Asp	aat Asn	tgc Cys 115	tac Tyr	cag Gln	ttc Phe	tat Tyr	aaa Lys 120	gac Asp	agc Ser	447
aaa Lys	agt Ser	tgg Trp 125	gag Glu	gac Asp	tgt Cys	aaa Lys	tat Tyr 130	ttc Phe	tgc Cys	ctt Leu	agt Ser	gaa Glu 135	aac Asn	tct Ser	acc Thr	495
atg Met	ctg Leu 140	aag Lys	ata Ile	aac Asn	aaa Lys	caa Gln 145	gaa Glu	gac Asp	ctg Leu	gaa Glu	ttt Phe 150	gcc Ala	gcg Ala	tct Ser	cag Gln	543
agc Ser 155	tac Tyr	tct Ser	gag Glu	ttt Phe	ttc Phe 160	tac Tyr	tct Ser	tat Tyr	tgg Trp	aca Thr 165	Gly aaa	ctt Leu	ttg Leu	cgc Arg	cct Pro 170	591
gac Asp	agt Ser	ggc Gly	aag Lys	gcc Ala 175	tgg Trp	ctg Leu	tgg Trp	atg Met	gat Asp 180	gga Gly	acc Thr	cct Pro	ttc Phe	act Thr 185	tct Ser	639
				att Ile												687
tgt Cys	gtg Val	gcc Ala 205	atc Ile	ctt Leu	aat Asn	ggg ggg	atg Met 210	atc Ile	ttc Phe	tca Ser	aag Lys	gac Asp 215	tgc Cys	aaa Lys	gaa Glu	735
				gtc Val												783
				ccc Pro									tga	ttcg	ccc	832
tct	gcaa	cta	caaa	tagc	ag a	gtga	gcca	g gc	ggtg	ccaa	agc	aagg	gct	agtt	gagaca	892
ttg	ggaa	atg	gaac	ataa	tc a	ggaa	agac	t at	ctct	ctga	cta	gtac	aaa	atgg	gttctc	952
gtg	tttc	ctg	ttca	ggat	ca c	cagc	attt	c tg	agct	tggg	ttt	atgc	acg	tatt	taacag	1012
tca	caag	aag	tctt	attt	ac a	tgcc	acca	a cc	aacc	tcag	aaa	ccca	taa	tgtc	atctgc	1072
ctt	cttg	gct	taga	gata	ac t	ttta	gctc	t ct	ttct	tctc	aat	gtct	aat	atca	cctccc	1132
tgt	tttc	atg	tctt	cctt	ac a	cttg	gtgg	a at	aaga	aact	ttt	tgaa	gta	gagg	aaatac	1192
att	gagg	taa	catc	cttt	tc t	ctga	cagt	c aa	gtag	tcca	tca	gaaa	ttg	gcag	tcactt	1252
ccc	agat	tgt	acca	gcaa	at a	caca	agga	a tt	cttt	ttgt	ttg	tttc	agt	tcat	actagt	1312
ccc	ttcc	caa	tcca	tcag	ta a	agac	ccca	t ct	gcct	tgtc	cat	gccg	ttt	ccca	acaggg	1372
atg	tcac	ttg	atat	gaga	at c	tcaa	atct	c aa	tgcc	ttat	aag	catt	cct	tcct	gtgtcc	1432

attaaqactc tgataattgt ctcccctcca taggaatttc tcccaggaaa gaaatatatc 1492 1552 cccatctccg tttcatatca gaactaccgt ccccgatatt cccttcagag agattaaaga ccagaaaaaa gtgagcctct tcatctgcac ctgtaatagt ttcagttcct attttcttcc 1612 attgacccat atttatacct ttcaggtact gaagatttaa taataataaa tgtaaatact 1672 1732 gtgaagtgtg tgtgatttta caatggactt atggttggtg ggaaaattca gcatggaaat gcttttcaaa atatgatagc ggtcattatt ttgattgtgc cttactgaaa gtttttgggg 1792 1852 aatttacaaq aqtactqatt acatqattat ctqqaqaaaa taagatqtct.thqaaataca tgttggcttc aagaaaacag ttttaacgtt ttcctaaaat gaaatctttt gaggtgagct 1912 tatggcatca acacatggtt gatgaggaag ctgagttgca ttagtgcaca tgatttccag 1972 tcaggtcatg ggaaatgaac agagacagtg acatctttgt agctgctcct ttgtgaggca 2032 2092 cttctttctt qaqatqactc catgcacaaa tataacaggg atcattggga atgacaccat 2125 cacagecace aagnttattg ggttactgat aat

247 <211> <212> PRT <213>

Homo sapiens

<220> <221>

misc_feature

<223> n = a or c or g or t

<400> 27

<210> 27

Met Gln Ala Lys Tyr Ser Ser Thr Arg Asp Met Leu Asp Asp Asp Gly

Asp Thr Thr Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr Arg His

Pro Glu Pro Arg Arg Thr Val Phe Gln Tyr Tyr Gln Leu Ser Asn Thr

Gly Gln Asp Thr Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr Ser

Gln Glu Leu Gln Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly Ser 70 75

Leu Gln His Val Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys Ala 95

Gly Ala His Arg Cys Ser Pro Cys Thr Glu Gln Trp Lys Trp His Gly 100

Asp	Asn	Cys 115	Tyr	Gln	Phe	Tyr	Lys 120	Asp	Ser	Lys	Ser	Trp 125	Glu	Asp	Cys	
Lys	Tyr 130	Phe	Cys	Leu	Ser	Glu 135	Asn	Ser	Thr	Met	Leu 140	Lys	Ile	Asn	Lys	
Gln 145	Glu	Asp	Leu	Glu	Phe 150	Ala	Ala	Ser	Gln	Ser 155	Tyr	Ser	Glu	Phe	Phe 160	
Tyr	Ser	Tyr	Trp	Thr 165	Gly	Leu	Leu.	Arg	Pro 170	Asp	Ser	Gly	rys	Ala 175	Trp	
Leu	Trp	Met	Asp 180	Gly	Thr	Pro	Phe	Thr 185	Ser	Glu	Leu	Phe	His 190	Ile	Ile	
Ile	Asp	Val 195	Thr	Ser	Pro	Arg	Ser 200	Arg	Asp	Cys	Val	Ala 205	Ile	Leu	Asn	
Gly	Met 210	Ile	Phe	Ser	Lys	Asp 215	Cys	Lys	Glu	Leu	Lys 220	Arg	Cys	Val	Cys	
Glu 225	Arg	Arg	Ala	Gly	Met 230	Val	Lys	Pro	Glu	Ser 235	Leu	His	Val	Pro	Pro 240	
Glu	Thr	Leu	Gly	Glu 245	Gly	Asp										
<210 <211 <212 <213	l > ! 2 >]	28 5059 DNA Homo	sap	iens												
<220 <221 <222	L> (CDS (199) (:	2457)											
<400 cggg		28 aat 9	ggaa	ggag	aa g	gcgg	aatg	t gg	gagg	gctc	agg	ggga	tgt	ggga	gggacg	60
aacg	ggag	aag (gggg	agag	ag g	aaaa.	tcca	g tc	tccc	ctgg	ccg	agca	ttt	tttt	ttttgg	120
aagt	taat	agg	actg	atct	cc a	ggac	cagc	a ct	cttc	tccc	agc	cctt	agg	gtcc	tgctcg	180
gcca	aagg	cct	tccc	tgcc								cag Gln				231
		_	_	_	_	_	_	-	_	_	_	ttg Leu			_	279
												cag Gln 40			cgg Arg	327

ttc Phe	cgg Arg 45	ctg Leu	gct Ala	ggc Gly	ttc Phe	ccc Pro 50	agg Arg	aag Lys	ccc Pro	tac Tyr	gag Glu 55	ggc Gly	cgc Arg	gtg Val	gag Glu		375
ata Ile 60	cag Gln	cga Arg	gct Ala	ggt Gly	gaa Glu 65	tgg Trp	ggc Gly	acc Thr	atc Ile	tgc Cys 70	gat Asp	gat Asp	gac Asp	ttc Phe	acg Thr 75		423
ctg Leu	cag Gln	gct Ala	gcc Ala	cac His 80	atc Ile	ctc Leu	tgc Cys	cgg Arg	gag Glu 85	ctg Leu	ggc Gly	ttc Phe	aca Thr	gag Glu 90	gcc Ala		471
aca Thr	G]y																519
tgg Trp	ctg Leu	gac Asp 110	aac Asn	ttg Leu	agc Ser	tgc Cys	agt Ser 115	gly aaa	acc Thr	gag Glu	cag Gln	agt Ser 120	gtg Val	act Thr	gaa Glu		567
tgt Cys	gcc Ala 125	tcc Ser	cgg Arg	ggc Gly	tgg Trp	999 Gly 130	aac Asn	agt Ser	gac Asp	tgt Cys	acg Thr 135	cac His	gat Asp	gag Glu	gat Asp	•	615
gct Ala 140	g1y	gtc Val	atc Ile	tgc Cys	aaa Lys 145	gac Asp	cag Gln	cgc Arg	ctc Leu	cct Prc 150	ggc Gly	ttc Phe	tcg Ser	gac Asp	tcc Ser 155		663
	gtc Val																711
	ccc Pro																759
	gtg Val																807
	tgg Trp 205																855
	agc Ser																903
	cag Gln																951
	gcc Ala																999
	gcc Ala														cca Pro		1047
															tcg Ser		1095

aag Lys 300	cct Pro	cag Gln	gly ggg	gag Glu	gtc Val 305	cgt Arg	gtc Val	cgt Arg	cta Leu	aag Lys 310	ggc Gly	ggc Gly	gcc Ala	cac His	cct Pro 315	1143
gga Gly	gag Glu	ggc Gly	cgg Arg	gta Val 320	gaa Glu	gtc Val	ctg Leu	aag Lys	gcc Ala 325	agc Ser	aca Thr	tgg Trp	ggc Gly	aca Thr 330	gtc Val	1191
tgt Cys	tac Tyr	cgc Arg	aag Lys 335	tgg Trp	gac Asp	ctg Leu	cat His	gca Ala 340	gcc Ala	agc Ser	gtg Val	gtg Val	tgt Cys 345	cgg Arg	gag Glu	1239
ctg. Leu	ggc Gly	ttc Phe 350	gly ggg	agt Ser	gct Ala	cga Arg	gaa Glu 355	gct Ala	ctg Leu	agt Ser	ggc Gly	gct Ala 360	cgc Arg	atg Met	gly ggg	1287
	ggc Gly 365															1335
gag Glu 380	ctc Leu	tcc Ser	ctc Leu	tgg Trp	aag Lys 385	tgc Cys	ccc Pro	cac His	aag Lys	aac Asn 390	atc Ile	aca Thr	gct Ala	gag Glu	gat Asp 395	1383
	tca Ser															1431
gly aaa	gca Ala	gag Glu	acc Thr 415	agg Arg	atc Ile	cga Arg	ctc Leu	agt Ser 420	gly aaa	ggc Gly	cgc Arg	agc Ser	caa Gln 425	cat His	gag Glu	1479
glà aaa	cga Arg	gtc Val 430	gag Glu	gtg Val	caa Gln	ata Ile	999 Gly 435	gga Gly	cct Pro	gly aaa	ccc Pro	ctt Leu 440	cgc Arg	tgg Trp	ggc	1527
ct.c Leu	atc Ile 445	tgt Cys	gly aaa	gat Asp	gac Asp	tgg Trp 450	gly aaa	acc Thr	ctg Leu	gag Glu	gcc Ala 455	atg Met	gtg Val	gcc Ala	tgt Cys	1575
agg Arg 460	caa Gln	ctg Leu	ggt Gly	ctg Leu	ggc Gly 465	tac Tyr	gcc Ala	aac Asn	cac His	ggc Gly 470	ctg Leu	cag Gln	gag Glu	acc Thr	tgg Trp 475	1623
	tgg Trp															1671
				Glu											acc Thr	1719
															atc Ile	1767
															cag Gln	1815
gag Glu 540	acc Thr	gcc Ala	tac Tyr	atc Ile	gaa Glu 545	Asp	cgg Arg	ccc Pro	ctg Leu	cat His 550	Met	ttg Leu	tac Tyr	tgt Cys	gct Ala 555	1863

gcg Ala	gaa Glu	gag Glu	aac Asn	tgc Cys 560	ctg Leu	gcc Ala	agc Ser	tca Ser	gcc Ala 565	cgc Arg	tca Ser	gcc Ala	aac Asn	tgg Trp 570	ccc Pro	1911
tat Tyr	ggt Gly	cac His	cgg Arg 575	cgt Arg	ctg Leu	ctc Leu	cga Arg	ttc Phe 580	tcc Ser	tcc Ser	cag Gln	atc Ile	cac His 585	aac Asn	ctg Leu	1959
	cga Arg	_	_					-		_				_		2007
	gag Glu 605															2055
	atc Ile															2103
	ttc Phe															2151
	gag Glu															2199
	ctc Leu															2247
	aag Lys 685															2295
gaa Glu 700	gta Val	gca Ala	gag Glu	agt Ser	gac Asp 705	ttt Phe	acc Thr	aac Asn	aat Asn	gca Ala 710	atg Met	aaa Lys	tgt Cys	aac Asn	tgc Cys 715	2343
	tat Tyr															2391
	ttc Phe													Gly	cag Gln	2439
	agc Ser		Gln			taa	gtgc	cac	tgcc	ctct	gc a	aacc	acca	С		2487
tgg	cccc	taa	tggc	aggg	gt c	tgag	gctg	c ca	ttac	ctca	gga	gctt	acc	aaga	aaccca	2547
tgt	cagc	aac	cgca	ctca	tc a	gacc	atgc	a ct	atgg	atgt	gga	actg	tca	agca	gaagtt	2607
ttc	accc	tcc	ttca	gagg	cc a	gctg	tcag	t at	ctgt	agcc	aag	catg	gga	atct	ttgctc	2667
сса	ggcc	cag	cacc	gagc	ag a	acag	acca	g ag	ccca	ccac	acc	acaa	aga	gcag	cacctg	2727
act	aact	gcc	caca	aaag	at g	gcag	cagc	t ca	tttt	cttt	aat	agga	ggt	cagg	atggtc	2787
agc	tcca	gta	tctc	ccct	aa g	ttta	<u>a</u> gaa	g at	acag	cttt	acc	tcta	gcc	tttt	ggtggg	2847

ggaaaagatc	cagccctccc	acctcatttt	ttactataat	atgttgctag	gtataatttt	2907
attttatata	aaaagtgttt	ctgtgattct	tcagagccca	ggagtcagtg	ctggtggttg	2967
gagggacctg	ccccactgg	ttcatttaac	cctctgtctc	ggtgccctca	gaacctcagc	3027
cagaaaggca	aggaggaaat	cagagcagga	gcctcatact	cttggtgatc	tattcattct	3087
gtgacctcag	gggtcacata	taaggtcagt	gtttctcgtc	cccgccggat	ctgcactgcc	3147
aactgggatt	gggttcgaac	agcttcataa	acatcttcag	cattttgtac	catctgctcc	3207
ccaatggcca	aaatcacatc	accaggccgc	agaccagccc	ggtgtgcagg	ggagcccagg	3267
atgactttat	ggatgagtac	accatgctga	acatcgggaa	agcttggttc	tcgaagctgt	3327
agttcagcaa	ggatgctggg	actcagggtc	agcatcatca	ccccaatgta	gcgccgctgg	3387
gacccactga	ttccggagga	ggaattcttc	tttcccccac	gatgcagaaa	ctctcgaaga	3447
cgatcagaag	ggatggcaaa	ggagattcca	gctgtgacct	tcatggtgtt	cactccaatc	3507
acctccccat	ccaggttaac	caggggacct	ccagagtttc	caaaatcaat	agctgcatca	3567
gtttgaatgt	attccacatt	ggtttggggg	agtcccaggt	ctctggctgg	acgctgagca	3627
gagctaacaa	tgccggatgt	gatcgtgttc	tgcagtgcaa	agggacttcc	catggcaaca	3687
acaaactccc	cttgccggac	atcagctgag	cgtcccagag	gcagcgtggg	gagaggetee	3747
ttagtctgaa	tecteagegt	tgcgatgtct	gccacgggat	ccacagctgt	gaccacggcc	3807
tcatacgtgt	cgccgcttag	cagtctcaca	cggactctgc	gccgatcagc	caccacatgg	3867
gcgttggtga	caatgagccc	atcggcagcc	accacgaatc	ctgagccgtt	cgagataggg	3927
acctcgcggc	ccaagaaagg	gtgccggtcc	aggatetega	tatagaccac	ggcaggtgct	3987
gtcttctcca	ccacatctgc	gatgaagttg	tactgactcc	ggggagaagc	gggcggcggg	4047
ctagggacgg	cggcgaggac	ggccggagga	ccccgacccc	cgccccacaa	caacaacagc	4107
actgcccccc	cagegeecag	cgccaccgcc	agccacgcgc	gcgaacgggt	tccagagttc	4167
tctgaggcct	cccgggtcct	ggtatctggg	gtcaccgcag	tcagttgtgc	ccggggaccc	4227
ggggtcccag	acgtcaggca	tgctcggggt	tcagtgaccc	caacagacaa	ccgggcccag	4287
agactggggg	tcccataagt	cactcgggcc	cgggggtcag	aagttcctga	cgtcagcagg	4347
gcccggaggt	caggggtcaa	acggggtctc	ctcccccagc	gaatgccccc	caaagcccgc	4407
catgcccgaa	ggctccagcc	tgcaccccgc	cccgccctcg	gcgcagccat	cageteegee	4467
ttggctgcct	cctcgcccgc	cctactcaga	ggcggcaccc	aggacgcgag	caggcggaca	4527
gtaggacgcg	gggcacgccg	gtacctgaag	tccttcagaa	gtgcacgccg	ggaccaggat	4587
tccgggaggc	cgactcctcc	ctgccccacg	aatgccggga	attgtggtct	ccgccggacg	4647
cgagttgtga	gacggcccaa	ggggccgcgg	ggtatgctgg	gaccgctagc	cattacggag	4707
cgcctcagga	cttcgggtcc	cctcaccccg	ggcggatgcc	caaagactcc	gccttcccaa	4767

gagcccctgc	ggccgggcgc	gaaaatggcg	gcggcggcga	cggccgggcg	ctcctgaagc	4827
agcagttatg	gagcttccct	cagggccggg	gccggagcgg	ctctttgact	cgcaccggta	4887
agagacccgg	cgggaagaga	ccgatccccg	cgtgctctcg	gccttcggcg	cctgaccact	4947
tegeeteteg	cccccaggct	tccgggtgac	tgcttcctac	tgctcgtgct	gctgctctac	5007
gcgccagtcg	ggttctgcct	cctcgtcctg	cgcctctttc	tcgggatcca	cg	5059

<210> 29 <211> 753 <212> PRT

<213> Homo sapiens

<400> 29

Met Arg Pro Val Ser Val Trp Gln Trp Ser Pro Trp Gly Leu Leu

Cys Leu Leu Cys Ser Ser Cys-Leu Gly Ser Pro Ser Pro Ser Thr Gly 20

Pro Glu Lys Lys Ala Gly Ser Gln Gly Leu Arg Phe Arg Leu Ala Gly

Phe Pro Arg Lys Pro Tyr Glu Gly Arg Val Glu Ile Gln Arg Ala Gly

Glu Trp Gly Thr Ile Cys Asp Asp Phe Thr Leu Gln Ala Ala His

Ile Leu Cys Arg Glu Leu Gly Phe Thr Glu Ala Thr Gly Trp Thr His 85

Ser Ala Lys Tyr Gly Pro Gly Thr Gly Arg Ile Trp Leu Asp Asn Leu

Ser Cys Ser Gly Thr Glu Gln Ser Val Thr Glu Cys Ala Ser Arg Gly 120

Trp Gly Asn Ser Asp Cys Thr His Asp Glu Asp Ala Gly Val Ile Cys

Lys Asp Gln Arg Leu Pro Gly Phe Ser Asp Ser Asn Val Ile Glu Val 145 150 155

Glu His His Leu Gln Val Glu Glu Val Arg Ile Arg Pro Ala Val Gly

Trp Gly Arg Arg Pro Leu Pro Val Thr Glu Gly Leu Val Glu Val Arg

185 190 180 Leu Pro Asp Gly Trp Ser Gln Val Cys Asp Lys Gly Trp Ser Ala His 205 195 200 Asn Ser His Val Val Cys Gly Met Leu Gly Phe Pro Ser Glu Lys Arg 215 Val Asn Ala Ala Phe Tyr Arg Leu Leu Ala Gln Arg Gln Gln His Ser 235 Phe Gly Leu His Gly Val Ala Cys Val Gly Thr Glu Ala His Leu Ser Leu Cys Ser Leu Glu Phe Tyr Arg Ala Asn Asp Thr Ala Arg Cys Pro 265 Gly Gly Pro Ala Val Val Ser Cys Val Pro Gly Pro Val Tyr Ala Ala Ser Ser Gly Gln Lys Lys Gln Gln Gln Ser Lys Pro Gln Gly Glu Val Arg Val Arg Leu Lys Gly Gly Ala His Pro Gly Glu Gly Arg Val Glu Val Leu Lys Ala Ser Thr Trp Gl; Thr Val Cys Tyr Arg Lys Trp 330 335

· 41

Harry Cont. Street

Many Many Harly

Asp Leu His Ala Ala Ser Val Val Cys Arg Glu Leu Gly Phe Gly Ser 340 345 350

Ala Arg Glu Ala Leu Ser Gly Ala Arg Met Gly Gln Gly Met Gly Ala 355 360 365

Ile His Leu Ser Glu Val Arg Cys Ser Gly Gln Glu Leu Ser Leu Trp 370 375 380

Lys Cys Pro His Lys Asn Ile Thr Ala Glu Asp Cys Ser His Ser Gln 385 390 395 400

Asp Ala Gly Val Arg Cys Asn Leu Prc Tyr Thr Gly Ala Glu Thr Arg 405 410 415

Ile Arg Leu Ser Gly Gly Arg Ser Gln His Glu Gly Arg Val Glu Val 420 425 430

Gln Ile Gly Gly Pro Gly Pro Leu Arg Trp Gly Leu Ile Cys Gly Asp 435 440 445

Asp Trp Gly Thr Leu Glu Ala Met Val Ala Cys Arg Gln Leu Gly Leu 450 460

Gly Tyr Ala Asn His Gly Leu Gln Glu Thr Trp Tyr Trp Asp Ser Gly 470 475 480

Asn Ile Thr Glu Val Val Met Ser Gly Val Arg Cys Thr Gly Thr Glu 485 490 495

Leu Ser Leu Asp Gln Cys Ala His His Gly Thr His Ile Thr Cys Lys 500 505 510

Arg Thr Gly Thr Arg Phe Thr Ala Gly Val Ile Cys Ser Glu Thr Ala 515 520 525

Ser Asp Leu Leu His Ser Ala Leu Val Gln Glu Thr Ala Tyr Ile 530 535 540

Glu Asp Arg Pro Leu His Met Leu Tyr Cys Ala Ala Glu Glu Asn Cys 545 550 555

Leu Ala Ser Ser Ala Arg Ser Ala Asn Trp Pro Tyr Gly His Arg Arg
565 570 575

Leu Leu Arg Phe Ser Ser Gln Ile His Asn Leu Gly Arg Ala Asp Phe 580 585 590

Arg Pro Lys Ala Gly Arg His Ser Trp Val Trp His Glu Cys His Gly 595 600 605

His Tyr His Ser Met Asp Phe Phe Thr His Tyr Asp Ile Leu Thr Pro 610 620

Asn Gly Thr Lys Val Ala Glu Gly His Lys Ala Ser Phe Cys Leu Glu 625 630 635 640

Asp Thr Glu Cys Gln Glu Asp Val Ser Lys Arg Tyr Glu Cys Ala Asn 645 650 655

Phe Gly Glu Gln Gly Ile Thr Val Gly Cys Trp Asp Leu Tyr Arg His

Asp Ile Asp Cys Gln Trp Ile Asp Ile Thr Asp Val Lys Pro Gly Asn 675 680 685

Tyr Ile Leu Gln Val Val Ile Asn Pro Asn Phe Glu Val Ala Glu Ser 690 695 700

Asp Phe Thr Asn Asn Ala Met Lys Cys Asn Cys Lys Tyr Asp Gly His 705 710 715

Arg Ile Trp Val His Asn Cys His Ile Gly Asp Ala Phe Ser Glu Glu 725 730 735

Ala Asn Arg Arg Phe Glu Arg Tyr Pro Gly Gln Thr Ser Asn Gln Ile 740 745 750

Ile

<2.10>

<211> 4552 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (127)..(1950) gggagagagg ggggtccagt ctcccctggc cgagcatttt ttttttggaa gtcctaggac 60 taatctccaq gaccagcact cttctcccag cccttagggt cctgctcggc caaggccttc 120 168 cetgee atg ega eet gte agt gte tgg eag tgg age eee tgg ggg etg Met Arg Pro Val Ser Val Trp Gln Trp Ser Pro Trp Gly Leu ctg ctg tgc ctg ctg tgc agt tcg tgc ttg ggg tct cca tcc cct tcc 216 Leu Leu Cys Leu Leu Cys Ser Ser Cys Leu Gly Ser Pro Ser Pro Ser 15: 264 acg ggc cct gag aag aag gcc ggg agc cag ggg ctt cgg ttc cgg ctg Thr Gly Pro Glu Lys Lys Ala Gly Ser Gln Gly Leu Arg Phe Arg Leu 312 gct ggc ttc ccc agg aag ccc tac gag ggc cgc gtg gag ata cag cga Ala Gly Phe Pro Arg Lys Pro Tyr Glu Gly Arg Val Glu Ile Gln Arg 360 gct ggt gaa tgg ggc acc atc tgc gat gat gac ttc acg ctg cag gct Ala Gly Glu Trp Gly Thr Ile Cys Asp Asp Asp Phe Thr Leu Gln Ala 408 gcc cac atc ctc tgc cgg gag ctg ggc ttc aca gag gcc aca ggc tgg Ala His Ile Leu Cys Arg Glu Leu Gly Phe Thr Glu Ala Thr Cly Trp 456 acc cac agt gcc aaa tat ggc cct gga aca ggc cgc atc tgg ctg gac Thr His Ser Ala Lys Tyr Gly Pro Gly Thr Gly Arg Ile Trp Leu Asp 504 aac ttg agc tgc agt ggg acc gag cag agt gtg act gaa tgt gcc tcc

Asn	Leu	Ser	Cys	Ser 115	Gly	Thr	Glu	Gln	Ser 120	Val	Thr	Glu	Cys	Ala 125	Ser	
cgg Arg	ggc Gly	tgg Trp	999 Gly 130	aac Asn	agt Ser	gac Asp	tgt Cys	acg Thr 135	cac His	gat Asp	gag Glu	gat Asp	gct Ala 140	gly aaa	gtc Val	552
	tgc Cys															600
	gcc Ala 160															648
_	gaa Glu	-	_	_	-	_					_	_	_		_	696
	gac Asp															744
	gct Ala															792
	atc Ile															840
	aag Lys 240	-			_				_			_			-	888
-	gat Asp	_		_		_							_			936
	atc Ile															984
	caa Gln														ggg Gly	1032
	gac Asp															1080
_	ggc Gly 320		_				_	_						-		1128
	aat Asn						_	_			_	_				1176
	ctg Leu		_	-	_	_	_								-	1224

					acc Thr												1272
	gca Ala				ttg Leu												1320
		-	-		ccc Pro			_	_		_	-		_			1368
	tgc Cys 415				tca Ser												1416
					ttc Phe 435												1464
A Section of the Sect				_	gct Ala		_								-		1512
of the first from the first					agc Ser	_	_						-				1560
Graff State State					aag Lys												1608
					tgt Cys												1656
					caa Gln 515												1704
	cat His				tgt Cys												1752
					cag Gln	_	_			,			_	_	_	~ _	1800
	agt				aac Asn												1848
					gtg Val												1896
					agg Arg 595												1944
		atc Ile	taaq	gtgc	cac 1	zgac	ctct	gc aa	aacca	acca	c tgg	gada	ctaa	tgg	cagg	ggt	2000

and the state an

ctgaggctgc	cattacctca	ggagcttacc	aagaaaccca	tgtcagcaac	cgcactcatc	2060
agaccatgca	ctatggatgt	ggaactgtca	agcagaagtt	ttcaccctcc	ttcagaggcc	2120
agctgtcagt	atctgtagcc	aagcatggga	atctttgctc	ccaggcccag	caccgagcag	2180
aacagaccag	ageccaccac	accacaaaga	gcagcacctg	actaactgcc	cacaaaagat	2240
ggcagcagct	cattttcttt	aataggaggt	caggatggtc	agctccagta	tctcccctaa	2300
gtttaggggg	atacagcttt	acctctagcc	ttttggtggg	ggaaaagatc	cagccctccc	2360
acctcatttt	ttactataat	atgttgctag	gtataatttt	attttatata	aaaagtgttt	2420
ctgtgattct	tcagagccca	ggagtcagtg	ctggtggttg	gagggacctg	ccccactgg	2480
ttcatttaac	cctctgtctc	ggtgccctca	gaacctcagc	cagaaaggca	aggaggaaat	2540
cagagcagga	gcctcatact	cttggtgatc	tattcattct	gtgacctcag	gggtcacata	2600
taaggtcagt	gtttctcgtc	cccgccggat	ctgcactgcc	aactgggatt	gggttcgaac	2660
agcttcataa	acatcttcag	cattttgtac	catctgctcc	ccaatggcca	aaatcacatc	2720
accaggccgc	agaccagccc	ggtgtgcagg	ggagcccagg	atgactttat	ggatgagtac	2780
accatgctga	acatcgggaa	agcttggttc	tcgaagctgt	agttcagcaa	ggatgctggg	2840
actcagggtc	agcatcatca	ccccaatgta	gcgccgctgg	gacccactga	ttccggagga	2900
ggaattcttc	ttttccccac	gatgcagaaa	ctctcgaaga	cgatcagaag	ggatggcaaa	2960
ggagattcca	gctgtgacct	tcatggtgtt	cactccaatc	acctccccat	ccaggttaac	3020
caggggacct	ccagagtttc	caaaatcaat	agctgcatca	gtttgaatgt	attccacatt	3080
ggtttggggg	agtcccaggt	ctctggctgg	acgctgagca	gagctaacaa	tgccggatgt	3140
gatcgtgttc	tgcagtgcaa	agggacttcc	catggcaaca	acaaactccc	cctgccggac	3200
atcagctgag	cgtcccagag	gcagcgtggg	gagaggetee	ttagtctgaa	tectcagegt	3260
tgcgatgtct	gccacgggat	ccacagctgt	gaccacggcc	tcatacgtgt	cgccgcttag	3320
cagtctcaca	cggactctgc	gccgatcagc	caccacatgg	gcgttggtga	caatgagccc	3380
atcggcagcc	accacgaatc	ctgagccgtt	cgagataggg	acctcgcggc	ccaagaaagg	3440
gtgccggtcc	aggatctcga	tatagaccac	ggcaggtgct	gtcttctcca	ccacatctgc	3500
gatgaagttg	tactgactcc	ggggagaagc	gggcggcggg	ctagggacgg	cggcgaggac	3560
ggccggagga	ccccgacccc	cgccccacaa	caacaacagc	actgcccccc	cagegeeeag	3620
cgccaccgcc	agccacgcgc	gcgaacgggt	tccagagttc	tctgaggcct	cccgggtcct	3680
ggtatctggg	gtcaccgcag	tcagttgtgc	ccggggaccc	ggggtcccag	acgtcaggca	3740
tgctcggggt	tcagtgaccc	caacagacaa	ccgggcccag	agactggggg	tcccataagt	3800
cactcgggcc	cgggggtcag	aagttcctga	cgtcagcagg	gcccggaggt	caggggtcaa	3860
acggggtctc	ctccccagc	gaatgccccc	caaagcccgc	catgcccgaa	ggctccagcc	3920

II

L

tqcaccccqc cccqccctcq gcgcagccat cagctccgcc ttggctgcct cctcgcccgc 3980 cctactcaga ggcggcaccc aggacgcgag caggcggaca gtaggacgcg gggcacgccg 4040 gtacctgaag teetteagaa gtgeaegeeg ggaeeaggat teegggagge egaeteetee 4100 ctgccccacg aatgccggga attgtggtct ccgccggacg cgagttgtga gacggcccaa ggggccgcgg ggtatgctgg gaccgctagc ccttccggcg cgcctcagga cttcgggtcc 4220 cctcaccccg ggcggatgcc caaagactcc gccttcccaa gagcccctgc ggccgggcgc 4280 gaaaatggcq gcggcggcga .cggccgggcg ctcctgaagc agcagttatg gagcttccct 4340 cagggccggg gccggagcgg ctctttgact cgcaccggta agagacccgg cgggaagaga 4400 cogatococy cytyctotocy goottoggog cotgacoact togoctotocy coccoagget 4460 4520 teegggtgae tgetteetae tgetegtget getgetetae gegeeagteg ggttetgeet cctcgtcctg cgcctctttc tcgggatcca cg 4552

<210> 31

<211> 608

PRT <212>

<213> Homo sapiens

<400> 31

.Met Arg Pro Val Ser Val Trp Gln Trp Ser Pro Trp Gly Leu Leu սeu

Cys Leu Leu Cys Ser Ser Cys Leu Gly Ser Pro Ser Pro Ser Thr Cly 2.0

Pro Glu Lys Lys Ala Gly Ser Gln Gly Leu Arg Phe Arg Leu Ala Gly 35

Phe Pro Arg Lys Pro Tyr Glu Gly Arg Val Glu Ile Gln Arg Ala Gly

Glu Trp Gly Thr Ile Cys Asp Asp Phe Thr Leu Gln Ala Ala His

Ile Leu Cys Arg Glu Leu Gly Phe Thr Glu Ala Thr Gly Trp Thr His

Ser Ala Lys Tyr Gly Pro Gly Thr Gly Arg Ile Trp Leu Asp Asn Leu 100

Ser Cys Ser Gly Thr Glu Gln Ser Val Thr Glu Cys Ala Ser Arg Gly 115

Trp Gly Asn Ser Asp Cys Thr His Asp Glu Asp Ala Gly Val Ile Cys

The state and the first term of the state of

	Lys 145	Asp	Gln	Arg	Leu	Pro 150	Gly	Phe	Ser	Asp	Ser 155	Asn	Val	Ile	Glu	Ala 160
	Arg	Val	Arg	Leu	Lys 165	Gly	Gly	Ala	His	Pro 170	Gly	Glu	Gly	Arg	Val 175	Glu
	Val	Leu	Lys	Ala 180	Ser	Thr	Trp	Gly	Thr 185	Val	Cys	Asp	Arg	Lys 190	Trp	Asp
	Leu	His	Ala 195	Ala	Ser	Val	Val	Cys 200	Arg	Glu	Leu	Gly	Phe 205	Gly	Ser	Ala
	Arg	Glu 210	Ala	Leu	Ser	Gly	Ala 215	Arg	Met	Gly	Gln	Gly 220	Met	Gly	Ala	Ile
	His 225	Leu	Ser	Glu	Val	Arg 230	Cys	Ser	Gly	Gln	Glu 235	Leu	Ser	Leu	Trp	Lys 240
	Cys	Pro	His	Lys	Asn 245	Ile	Thr	Ala	Glu	Asp 250	Cys	Ser	His	Ser	Gln 255	Asp
:	Ala	Gly	Val	Arg 260	Cys	Asn	Leu	Pro	Tyr 265	Thr	Gly	Ala	Glu	Thr 270	Arg	Ile
1	Arg	Leu	Ser 275	Gly	Gly	Arg	Ser	Gln 280	His	Glu	Gly	Arg	Val 285	Glu	Val	Gln
	Ile	Gly 290	Gly	Pro	Gly	Pro	Leu 295	Arg	Trp	Gly	Leu	Ile 300	Cys	Gly	Asp	Asp
	Trp 305	Gly	Thr	Leu	Glu	Ala 310	Met	Val	Ala	Cys	Arg 315	Gln	Leu	Gly	Leu	Gly 320
	:. Tyr	Ala	Asn	His	Gly 325	Leu	Gln	Glu	Thr	Trp 330	Tyr	Trp	Asp	Ser	Gly 335	Asn
	Ile	Thr	Glu	Val 340	Val	Met	Ser	Gly	Val 345	Arg	Cys	Thr	Gly	Thr 350	Glu	Leu
	Ser	Leu	Asp 355	Gln	Cys	Ala	His	His 360	Gly	Thr	His	Ile	Thr 365	Cys	Lys	Arg
	Thr	Gly 370	Thr	Arg	Phe	Thr	Ala 375	Gly	Val	Ile	Cys	Ser 380	Glu	Thr	Ala	Ser

Asp Leu Leu Leu His Ser Ala Leu Val Gln Glu Thr Ala Tyr Ile Glu 385 390 395 400

Asp Arg Pro Leu His Met Leu Tyr Cys Ala Ala Glu Glu Asn Cys Leu \$405\$ \$410\$ \$415

Ala Ser Ser Ala Arg Ser Ala Asn Trp Pro Tyr Gly His Arg Arg Leu 420 425 430

Leu Arg Phe Sec Ser Gln Ile His Asn Leu Gly Arg Ala Asp Fhe Arg 435 440 445

Pro Lys Ala Gly Arg His Ser Trp Val Trp His Glu Cys His Gly His 450 455 460

Tyr His Ser Met Asp Phe Phe Thr His Tyr Asp Ile Leu Thr Pro Asn 465 470 470 475 475

Gly Thr Lys Val Ala Glu Gly His Lys Ala Ser Phe Cys Leu Glu Asp \$485\$

Thr Glu Cys Gln Glu Asp Val Ser Lys Arg Tyr Glu Cys Ala Asn Phe 500 505 510

Gly Glu Gln Gly Ile Thr Val Gly Cys Trp Asp Leu Tyr Arg His Asp 515 520 525

Ile Asp Cys Gln Trp Ile Asp Ile Thr Asp Val Lys Fro Gly Asn Tyr 530 535 540

Ile Leu Gln Val Val Ile Asn Pro Asn Phe Glu Val Ala Glu Ser Asp 545 550 560

Phe Thr Asn Asn Ala Met Lys Cys Asn Cys Lys Tyr Asp Gly His Arg 565 570 575

Ile Trp Val His Asn Cys His Ile Gly Asp Ala Phe Ser Glu Glu Ala 580 585 590

Asn Arg Arg Phe Glu Arg Tyr Pro Gly Gln Thr Ser Asn Gln Ile Ile 595 600 605

<210> 32

<211> 16545

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (862)..(14769)

<400> 32						
	ccccagagaa	aaacgctgc	c aattegttge	tttattgttc	ectgcctggg	60
gacctcaata	gccttttcca	ttaaccttc	c cttcttacgc	aacggttaat	gactttgggg	120
gttgttttgc	tttctgtttc	tgctgagtca	a ctaaattttg	cctctttgtc	cccaggtgct	180
gctcagcata	aaagttaaaa	gtgcaattc	a ggaagtactg	ggattctgtg	tagagccgag	240
gaaaccattt	ccctaagaga	agctctgtt	c cttggcttgt	ccttccttcc	cçggaaggaa	300
gcttccgagg	aacgaaggga	gaagctttg	t tttgcctgca	gaagcagccc	tgtgctcggc	360
tgagggttct	cagctggctg	tgaactgcg	g agcattgtag	gegeetgget	ggctcaggcc	420
aatgcagaag	tctctccctt	ctccaaaga	c ccaaatcccc	acagaaccag	cttcgagtta	480
ctttcccttc	aaggggatta	aaataattg	t gatttgtggd	gctctccgtt	cgcggtggta	540
ttttcctgtt	gtgttaaatg	cctcttatt	a agtaatagat	gtgatttatg	tgaacgacga	600
aggggtgtgt	ggtggattcg	gtgattaat	c agtgaattcc	catccgctgg	catctctcac	660
tgcccctctt	gcgtgatgta	agatcagac	g taccctgcat	tgaaaagtca	agacacacgg	720
gcgtctcgct	cgcgctcaca	cacgetetg	c ctectetete	cagcacgcgc	gcatccctcc	780
accttccaca	tcctgctcca	ggcaggaga	a ggctgactgg	ctggactcat	tgagctgaag	840
aatttccagt	gacatttgta			tcc agg ctc Ser Arg Leu		891
				gtg ccg ccg Val Pro Pro		939
				atg tcc gag Met Ser Glu 40		987
-				att gcc agg Ile Ala Arg 55		1035
				gat cct ggt Asp Pro Gly 70		1083
	s Asp His V			agc tgg ctg Ser Trp Leu		1131
				tct tta gat Ser Leu Asp		1179
				cac att gct His Ile Ala 120	Cys Leu	1227

ggt acc acc aca tgg ggt tat gac gga gga gga gga acc acc ggg acc ggg acc gga acc acc		
Asp Cys Pro Asp Gly Tyr Asp Glu Gly Val His Cys Gln Gli 140 tcc aat tgc caa cag ctg aat tgt cag tat aaa tgt aca ats Ser Asn Cys Gln Gln His Ger Asn Cys Gln Gln His Ger Asn Cys Gln Gln Tyr Lys Cys Thr Mei 165 aat agt aca aga tgt tac tgt gag gat gga ttc gaa ata aca Asn Ser Thr Arg Cys Tyr Cys Glu Asp Gly Phe Glu Ile Thing Gly Arg Ser Cys Lys Asp Gln Asp Glu Cys Ala Val Tyr Gly 195 agc cag acc tgc aga aac aca cat gga tcc tac act tgc agg Ser Gln Thr Cys Arg Asn Thr His Gly Ser Tyr Thr Cys Ser 205 gaa ggc tac cta atg cag cac aca gac aca aga tct tgc aag Glu Gly Tyr Leu Met Gln Pro Asp Asn Arg Ser Cys Lys Ala 220 gaa cct aca gat aga cac ctt ata cta tta att gca aag tt gac Glu Gly Tyr Leu Met Gln Pro Asp Asn Arg Ser Cys Lys Ala 220 gaa cct aca gat aga cac ct ata cta tta att gca aat tt glu Pro Thr Asp Arg Pro Pro Ile Leu Leu Ile Ala Asn Phe 240 att gag gtt ttc tat ctt aat gga agt aaa atg ga act cta act tga Glu Pro Thr Asp Arg Pro Pro Ile Leu Leu Ile Ala Asn Phe 255 gtc aat gga aat gaa att cat act ctg gat ttt att aat Val Asn Gly Asn Glu Ile His Thr Leu Asp Phe Ile Tyr Asn 270 gtg att tgt gg att gaa tca aga gaa tct tca act cta act Val Asn Gly Asn Glu Ile Glu Ser Arg Glu Ser Ser Asn Glu Leu 285 gtc cag ata aca aaa gca gga gga tta aca atg gca act cta act tga ala cac aca cta val Asn Gly Asn Glu Ile Ser Arg Glu Ser Ser Asn Glu Leu 285 gtc aat tgt tgg att gaa tca aga gat ta aca gat gaa tcc aca act cta cac aca cta cac aca cta cac aca cac aca cac aca aca		275
Ser Asn Cys Gln Gln Leu Asn Cys Gln Tyr Lys Cys Thr Mei 155 aat agt aca aga tgt tac tgt gag gat gga ttc gaa ata aca Asn Ser Thr Arg Cys Tyr Cys Glu Asp Gly Phe Glu Ile Thr 175 ggg aga agc tgt aaa gat caa gat gaa tgt Cys Ala Val Tyr Gly 190 agc cag acc tgc aga aac aca cat gga tcc tac act tgc ag ser Gln Thr Cys Arg Asn Thr His Gly Ser Tyr Thr Cys Ser 210 gaa ggc tac cta atg cag cag aac aca aga tct tgc aag gaa ggu Gly Tyr Leu Met Gln Pro Asp Asn Arg Ser Cys Lys Ala 220 gaa cct aca gat aga cca ct ata cta tta att gca aat tt ggu Phe Glu Ile Thr Cys Ser 210 gaa cct aca gat aga cca cct ata cta tta att gca aat tt ggu Phe Glu Ile Ile Glu Val Phe Tyr Leu Asn Gly Ser Lys Met Ala Thr Leu Asn Gly Asn Glu Ile His Thr Leu Asp Phe Ile Tyr Asn 270 gtg att tgt tgg att gaa tca aga gat tct tca aat cta tta tat att gar act tat and act act act and act and act		323
Asn Ser Thr Arg Cys Tyr Cys Glu Asp Gly Phe Glu Ile The 175 Tyr Cys Glu Asp Gly Phe Glu Ile The 180 Tyr Cys Lys Asp Gln Asp Glu Cys Ala Val Tyr Gly 190 Thr Cys Arg Asn Thr His Gly Ser Tyr Thr Cys Ser Cys Lys Arg Asn Thr His Gly Ser Tyr Thr Cys Ser Cys Lys Arg Asn Thr His Gly Ser Tyr Thr Cys Ser Cys Lys Arg Asn Thr His Gly Ser Tyr Thr Cys Ser Cys Lys Arg Asn Thr His Gly Ser Tyr Thr Cys Ser Cys Lys Arg Asn Thr His Gly Ser Tyr Thr Cys Ser Cys Lys Arg Cys Cys Lys Arg Cys Lys Arg Cys Cys Cys Cys Lys Arg Cys		371
Gly Arg Ser Cys Lys Asp Gln Asp Glu Cys Ala Val Tyr Gly 200 agc cag acc tgc aga aac aca cat gga tcc tac act tgc agg ser Gln Thr Cys Arg Asn Thr His Gly Ser Tyr Thr Cys Ser 215 gaa ggc tac cta atg cag cca gac aac aga tct tgc aag gcd Glu Gly Tyr Leu Met Gln Pro Asp Asn Arg Ser Cys Lys Ala 220 gaa cct aca gat aga cca cct ata cta tta att gca aat ttd Glu Pro Thr Asp Arg Pro Pro Ile Leu Leu Ile Ala Asn Pho 235 att gag gtt ttc tat ctt aat gga agt aaa atg gca act cta Ile Glu Val Phe Tyr Leu Asn Gly Ser Lys Met Ala Thr Leu 255 gtc aat gga aat gaa att cat act ctg gat ttt att tat aat Val Asn Gly Asn Glu Ile His Thr Leu Asp Phe Ile Tyr Asn 270 gtg att tgt tgg att gaa tca aga gaa tct tca aat caa ctc Val Ile Cys Trp Ile Glu Ser Arg Glu Ser Ser Asn Glu Leu 295 atc cag ata aca aaa gca gga gga tta aca ggt gaa tgaa ctc cag atc ctc Ile Gln Ile Thr Lys Ala Gly Gly Leu Thr Asp Glu Trp The Asp 300 att ctt caa tcc ttc cac aat gtg gac cat gtc ggt gac cgg atc ctc act cag aat ctc tat ttt gtg gac cat gtc ggt gac cgg atc cac cga aat ctc tat ttt gtg gac cat gtc ggt gac cgg atc cac cga aat ctc tat ttt gtg gac cat gtc ggt gac cgg atc cac cga aat ctc tat ttt gtg gac cat gtc ggt gac cgg atc cac cga aat ctc tat ttt gtg gac cat gtc ggt gac cgg atc cac cga aat ctc tat ttt gtg gac cat gtc ggt gac cgg atc cac cga atc cac cga ata cac ctc tat ttt gtg gac cat gtc ggt gac cgg atc cac cga atc cac cga atc ctc tat ttt gtg gac cat gtc ggt gac cgg atc cac cga atc cac cga atc cac cac cac cga atc cac cac cac cac cac cac cga atc cac cac cac cac cac cac cac cac ca		419
Ser Gln Thr Cys Arg Asn Thr His Gly Ser Tyr Thr Cys Ser 205 gaa ggc tac cta atg cag cca gac aac aga tct tgc aag gcf Glu Gly Tyr Leu Met Gln Pro Asp 225 gaa cct aca gat aga cca cct ata cta tta att gca aat tt Glu Pro Thr Asp Arg Pro Pro Ile Leu Leu Ile Ala Asn Pho 235 att gag gtt ttc tat ctt aat gga agt aaa atg gca act cta Ile Glu Val Phe Tyr Leu Asn Gly Ser Lys Met Ala Thr Leu 255 gtc aat gga aat gaa att cat act ctg gat ttt att tat aat Val Asn Gly Asn Glu Ile His Thr Leu 275 gtg att tgt tgg att gaa tca aga gga ttt tca aat caa ctc Val Ile Cys Trp Ile Glu Ser Arg Glu Ser Ser Asn Gln Leu 285 atc cag ata aca aca gga gga tta aca gat gaa tcg Ile Gln Ile Thr Lys Ala Gly Gly Leu Thr Asp Glu Trp Thr 300 att ctt caa tcc ttc cac aat gtg gac cat gtc ggt gac cgg atc Thr Arg Asn Leu Tyr Phe Val Asp His Val Gly Asp Arg Ile Cys Arg Ile Cya Asp Arg Ile Cya aat ctc tat ttt gtg gac cat gtc ggt gac cgg atc Cya Arg Arg Arg Arg Ile Cya Arg Asp Arg Ile Cya Arg Arg Asp Arg Ile Cya Arg	y Thr Cys	467
Glu Gly Tyr Leu Met Gln Pro Asp Asn Arg Ser Cys Lys Ala 220 gaa cct aca gat aga cca cct ata cta tta att gca aat tta Glu Pro Thr Asp Arg Pro Pro Ile Leu Leu Ile Ala Asn Pha 235 att gag gtt ttc tat ctt aat gga agt aaa atg gca act cta Ile Glu Val Phe Tyr Leu Asn Gly Ser Lys Met Ala Thr Leu 255 gtc aat gga aat gaa att cat act ctg gat ttt att tat aaa Val Asn Gly Asn Glu Ile His Thr Leu Asp Phe Ile Tyr Asi 270 gtg att tgt tgg att gaa tca aga gaa tct tca aat caa cta Val Ile Cys Trp Ile Glu Ser Arg Glu Ser Ser Asn Gln Leu 295 atc cag ata aca aaa gca gga gga tta aca gat gaa tgg aca Ile Gln Ile Thr Lys Ala Gly 305 att ctt caa tcc ttc cac aat gtg caa caa atg gcg att gac aca Ile Gln Ser Phe His Asn Val Gln Gln Met Ala Ile Asn 315 act cga aat ctc tat ttt gtg gac cat gtc ggt gac cgg att Arg Arg Ile Cya Arg Arg Ile Cya		515
Glu Pro Thr Asp Arg Pro 240 att gag gtt ttc tat ctt aat gga agt aaa atg gca act cta Ile Glu Val Phe Tyr Leu Asn Gly Ser Lys Met Ala Thr Leu 255 gtc aat gga aat gaa att cat act ctg gat ttt att tat aaa Val Asn Gly Asn Glu Ile His Thr Leu Asp Phe Ile Tyr Ass 275 gtg att tgt tgg att gaa tca aga gaa tct tca aat caa ctc Val Ile Cys Trp Ile Glu Ser Arg Glu Ser Ser Asn Gln Leu 290 atc cag ata aca aaa gca gga gga tta aca gat gaa tgg aca Ile Gln Ile Thr Lys Ala Gly Gly Leu Thr Asp Glu Trp The 300 att ctt caa tcc ttc cac aat gtg caa caa atg gcg att gac Ile Leu Gln Ser Phe His Asn Val Gln Gln Met Ala Ile Asn 315 act cga aat ctc tat ttt gtg gac cat gtc ggt gac cgg atc Thr Arg Asn Leu Tyr Phe Val Asp His Val Gly Asp Arg Ile		563
Ile Glu Val Phe Tyr Leu Asn Gly Ser Lys Met Ala Thr Leu 255 gtc aat gga aat gaa att cat act ctg gat ttt att tat aat Val Asn Gly Asn Glu Ile His Thr Leu Asp Phe Ile Tyr Asn 275 gtg att tgt tgg att gaa tca aga gaa tct tca aat caa ctc Val Ile Cys Trp Ile Glu Ser Arg Glu Ser Ser Asn Gln Leu 285 atc cag ata aca aaa gca gga gga tta aca gat gaa tgg aca Ile Gln Ile Thr Lys Ala Gly Gly Leu Thr Asp Glu Trp The 300 att ctt caa tcc ttc cac aat gtg caa caa atg gcg att gac Ile Leu Gln Ser Phe His Asn Val Gln Gln Met Ala Ile Asp 315 act cga aat ctc tat ttt gtg gac cat gtc ggt gac cgg atc Thr Arg Asn Leu Tyr Phe Val Asp His Val Gly Asp Arg Ile		611
Yal Asn Gly Asn Glu Ile His Thr Leu Asp Phe Ile Tyr Asn 270 275 286 gtg att tgt tgg att gaa tca aga gaa tct tca aat caa ctc Val Ile Cys Trp Ile Glu Ser Arg Glu Ser Ser Asn Gln Leu 295 atc cag ata aca aaa gca gga gga tta aca gat gaa tgg aca Ile Gln Ile Thr Lys Ala Gly Gly Leu Thr Asp Glu Trp The 300 305 305 310 att ctt caa tcc ttc cac aat gtg caa caa atg gcg att gac Ile Leu Gln Ser Phe His Asn Val Gln Gln Met Ala Ile Asp 315 320 325 act cga aat ctc tat ttt gtg gac cat gtc ggt gac cgg atc Thr Arg Asn Leu Tyr Phe Val Asp His Val Gly Asp Arg Ile	a agc tca 16 u Ser Ser 265	659
Val Ile Cys Trp Ile Glu Ser Arg Glu Ser Asn Gln Let 285 atc cag ata aca aaa gca gga gga tta aca gat gaa tgg aca Ile Gln Ile Thr Lys Ala Gly Gly Leu Thr Asp Glu Trp Thr 300 att ctt caa tcc ttc cac aat gtg caa caa atg gcg att gac Ile Leu Gln Ser Phe His Asn Val Gln Gln Met Ala Ile Asp 315 act cga aat ctc tat ttt gtg gac cat gtc ggt gac cgg atc Thr Arg Asn Leu Tyr Phe Val Asp His Val Gly Asp Arg Ile	n Glu Asp	707
Ile Gln Ile Thr Lys Ala Gly Gly Leu Thr Asp Glu Trp Thr 300 305 305 310 att ctt caa tcc ttc cac aat gtg caa caa atg gcg att gad Ile Leu Gln Ser Phe His Asn Val Gln Gln Met Ala Ile Asp 315 320 325 act cga aat ctc tat ttt gtg gac cat gtc ggt gac cgg atd Thr Arg Asn Leu Tyr Phe Val Asp His Val Gly Asp Arg Ile		755
Ile Leu Gln Ser Phe His Asn Val Gln Gln Met Ala Ile Asp 315 320 325 act cga aat ctc tat ttt gtg gac cat gtc ggt gac cgg atc Thr Arg Asn Leu Tyr Phe Val Asp His Val Gly Asp Arg Ile	a atc aat / 18 r Jle Asn	803
Thr Arg Asn Leu Tyr Phe Val Asp His Val Gly Asp Arg Ile		851
335 340	c ttt gtt 18 e Phe Val 345	899
tgt aat tcc aac ggt tct gta tgt gtc acc ctg att gat ctg Cys Asn Ser Asn Gly Ser Val Cys Val Thr Leu Ile Asp Leu 350 355 360	ı Glu Leu	947
cac aat cct aaa gca ata gca gta gat cca ata gca gga aaa His Asn Pro Lys Ala Ile Ala Val Asp Pro Ile Ala Gly Lys 365 370 375	a ctt ttc 19 s Leu Phe	995

						aaa Lys					2043
						gat Asp					2091
						aaa Lys					2139
						gac Asp 435					2187
						aga Arg					2235
	_	_		_	_	aat Asn	_			_	2283
			_			gat Asp					2331
						tat Tyr					2379
į						gat Asp 515					2427
						agc Ser					2475
						gga Gly					2523
						ttt Phe					2571
						acc Thr					2619
						cct Pro 595					2667
						gac Asp					2715
						aga Arg					2763

													gac Asp							2811
													acc Thr 660							2859
				-		_			_		-		ctt Leu				_	_		2907
:	.•												att Ile							2955
													gac Asp							3003
-		The state of the s		Lys 715	Āla	Trp	Met	Āsp	Gly 720	Phe	Asn	Arg	cag Gln	Ile 725	Phe	Val	Thr	Ser	Lys 730	3051
		THE STATE OF THE S		atg Met	ctg Leu	tgg Trp	cca Pro	aac Asn 735	ggt Gly	tta Leu	act Thr	ctg Leu	gac Asp 740	ttt Phe	cac His	acc Thr	aac Asn	aca Thr 745	tta Leu	3099
		The state of the s					_				_		att Ile	_		_		_		3147
													Gly aaa							3195
t e													gtg Val							3243
													ata Ile							3291
		ı		ctg Leu	agg Arg	cat His	gaa Glu	aga Arg 815	cca Pro	ccc Pro	cta Leu	ttt Phe	999 Gly 820	ctt Leu	cag Gln	att Ile	tat Tyr	gat Asp 825	cca Pro	3339
ı	2												cga Arg							3387
			•	agt Ser	aca Thr	ctt Leu 845	tgc Cys	ttg Leu	gct Ala	atc Ile	cca Pro 850	gga Gly	ggc Gly	cgg Arg	gtg Val	tgt Cys 855	gct Ala	tgt Cys	gcc Ala	3435
				gat Asp	aat Asn 860	caa Gln	ctt Leu	ttg Leu	gat Asp	gaa Glu 865	aat Asn	gly aaa	aca Thr	act Thr	tgc Cys 870	aca Thr	ttt Phe	aat Asn	cct Pro	3483
				gga Gly 875	gaa Glu	gca Ala	cta Leu	cct Pro	cac His 880	ata Ile	tgt Cys	aaa Lys	gct Ala	gga Gly 885	gag Glu	ttt Phe	cgc Arg	tgc Cys	aaa Lys 890	3531

											з Су						gac Asp	3579
														he A			agc Ser	3627
			gat Asp 925										rg C				aag Lys	3675
. •	Arg				-		_		_	_		y Se	-	-		-	gaa Glu	3723
												n Va					tct Ser 970	3771
					-	_			_	_	a Tr	_	_		_		gaa Glu	3819
The state of the s	~	_	tgt Cys		_			_	_	-				ýs (_	Ph	c cca le Pro	3867
Bridge death, gann			gag Glu 1005	Pro	cta Leu				e V				agt Ser		<i>Y</i> .	aga Arg	_	3912
		_	agc Ser 1020	Lys	tgg Trp				s S				gac Asp		3	ggg Gly	_	3957
THE STATE OF THE S		agt Ser	gat Asp 1035	Glu	gtg ı Val			_	L H				ttt Phe		٥.	aat Asn		4002
	_		tgt Cys 1050	Ser	agt Ser				3 I				cac His			gcc Ala	_	4047
	gat Asp	ggt Gly	gac Asp 1065	Asr	gac Asp	tgt Cys	g]} : gg9	gad Asi) P	tc a	agt Ser	gat Asp	gaa Glu	gco Ala 10	э.	cag Gln		4092
			act Thr 1080	Lys	a gaa Glu				s S						3 .			4137
			ttt Phe 1095	Glr	ı tgo ı Cys				G. G						Ο.	gat Asp		4182
	tgg Trp	cgc Arg	tgt Cys 1110	Asp	gga Gly	gaa Glu	aaa Lys	gad S Asp 111) C	gt g ys (gaa Glu	gat Asp	ggt Gly	agt Sei 112	r.	gat Asp	gaa Glu	4227
	aaa Lys	ggt Gly	tgc Cys 1125	Asr	ggt Gly				g L				cac His		3	acc Thr		4272

	ttt Phe	tcc Ser	tgt Cys 1140					aga Arg 1145							gtg Val	4317
	tgt Cys	gat Asp	gga Gly 1155	gat Asp	att Ile	gat Asp	tgc Cys	gaa Glu 1160	gat Asp	cag Gln	tca Ser	gat Asp	gaa Glu 1165	gat Asp	_	4362
	tgt Cys	gac Asp	agt Ser 1170	ttc Phe	ttg Leu	tgt Cys	gga Gly	cca Pro 1175	ccc Pro	aag Lys	cat His	cct Pro	tgt Cys 1180		aat Asn	4407
÷ .	gac Asp	acc Thr	tca Ser 1185	gcc Val	tgc Cys	ctg Leu	cag Gln	cca Pro 1190	gag Glu	aaa Lys	ctc Leu	tgc Cys	aət Asn 1195	Gl ^y 333	aaa Lys	4452
ï	aag Lys	gat Asp	tgt Cys 1200	cct Pro	gat Asp	ggc	tct Ser	gat Asp 1205	gaa Glu	ggc Gly	tat Tyr	ctc Leu	tgt Cys 1210		gag Glu	4497
And the second s	tgt Cys	tcg Ser	ctg Leu 1215	aac Asn	aat Asn	gga Gly	ggc Gly	tgt Cys 1220	agc Ser	aac Asn	cac His	tgt Cys	tct Ser 1225	gtt Val	gtt Val	4542
the fact with the fact the fac	cct Pro	gga Gly	aga Arg 1230	gga Gly	att Ile	gtc Val	tgt Cys	tcc Ser 1235	tgc Cys	cct Pro	gaa Glu	gga Gly	ctt Leu 1240	caa Gln		4587
The state of the s			gac Asp 1245					gaa Glu 1250					tgt Cys 1255	_	aat Asn	4632
								tgt Cys 1265							gtc Val	4677
Marie Paris Control of the Control o	aag Lys	tgc Cys	tca Ser 1275	tgt Cys	tat Tyr	gaa Glu	ggt Gly	tgg Trp 1280	aag Lys	ctg Leu	gat Asp	gta Val	gac Asp 1285	ggt Gly	gaa Glu	4722
	agt Ser	tgt Cys	aca Thr 1290	agt Ser	gtt Val	gat Asp	cct Pro	ttt Phe 1295	gaa Glu	gca Ala	ttc Phe	atc Ile	atc Ile 1300		tct Ser	4767
	att Ile	cgt Arg	cat His 1305	gag Glu	atc Ile	aga Arg	agg Arg	att Ile 1310	gat Asp	ctt Leu	cac His	aaa Lys	aga Arg 1315	gac Asp	tat Tyr	4812
	agt Ser	cta Leu	ctt Leu 1320	gtt Val	cct Pro	gga Gly	ttg Leu	aga Arg 1325	aac Asn	aca Thr	ata Ile	gca Ala	ctt Leu 1330	gat Asp		4857
*	các His	ttc Phe	aat Asn 1335	caa Gln	agt Ser	tta Leu	ctt Leu	tat Tyr 1340	tgg Trp	aca Thr	gat Asp	gtt Val	gta Val 1345	gaa Glu		4902
*	aga Arg	ata Ile	tac Tyr 1350	cgg Arg	gga Gly	aag Lys	ctt Leu	tct Ser 1355	gaa Glu	agt Ser	gga Gly	ggt Gly	gtc Val 1360	agt Ser	_	4947
	att Ile	gaa Glu	gtg Val 1365	gtt Val	gtg Val	gag Glu	cat His	ggc Gly 1370	ctg Leu	gct Ala	act Thr	cca Pro	gaa Glu 1375	ggc	_	4992

aca Thr	gtc Val	gac Asp 1380	tgg Trp	ata Ile	gca Ala	gga Gly	aac Asn 1385	ata Ile				gac Asp 1390			5037
ctg Leu	gac Asp	caa Gln 1395	atc Ile	gaa Glu	gtg Val	gcc Ala	aaa Lys 1400					cta Leu 1405			5082
aca Thr	cta Leu	ata Ile 1410	gca Ala	gga Gly	gcc Ala	atg Met	gaa Glu 1415	cac His	ccc Pro	agg Arg	gcc Ala	att Ile 1420	gct Ala	ttg Leu	5127
							ttc Phe 1430					gat Asp 1435			5172
							tct Ser 1445					999 Gly 1450			5217
acc Thr	atc Ile	tat Tyr 1455	aaa Lys	gac Asp	atg Met	aaa Lys	act Thr 1460	Gly ggg	gct Ala	tgg Trp	cct Pro	aat Asn 1465	gga Gly	cta Leu	5262
act Thr	gtg Val	gac Asp 1470	cac Hıs	ttt Phe	gag Glu	aaa Lys	agg Arg 1475					gac Asp 1480			5307
tca Ser	gat Asp	gct Ala 1485	att Ile	tat Tyr	tca Ser	gcc Ala	ctc Leu 1490					aac Asn 1495			5352
gaa Glu	atc Ile	atc Ile 1500	cga Arg	ggt Gly	cat His	gaa Glu	tac Tyr 1505	ctt Leu				ttt Phe 1510	gct Ala		5397
tçt Ser	cta Leu	tat Tyr 1515	Gly aaa	agt Ser	gaa Glu	gtc Val	tac Tyr 1520	tgg Trp	aca Thr	gac Asp	tgg Trp	agg Arg 1525	acc Thr		5442
aca Thr	ttg Leu	tcc Ser 1530	aaa Lys	gcc Ala	aat Asn	aag Lys	tgg Trp 1535					gtc Val 1540	agt Ser		5487
att	cag Gln	aaa Lys 1545	acc Thr	agt Ser	gca Ala	cag Gln	cca Pro 1550	ttt Phe	gac Asp	ctt Leu	cag Gln	ata Ile 1555	tac Tyr		5532
ccc Pro	agt Ser	cgc Arg 1560	cag Gln	cca Pro	cag Gln	gct Ala	ccc Pro 1565					gct Ala 1570			5577
	aaa Lys	ggc Gly 1575	ccc Pro	tgc Cys	tct Ser	cac His	atg Met 1580	tgt Cys	cta Leu	atc Ile	aat Asn	cac His 1585	aat Asn		5622
	gct Ala	gcc Ala 1590	tgt Cys	gcg Ala	tgc Cys	ccc Pro	cac His 1595					tct Ser 1600	tca Ser	_	5667
_	aag Lys						aaa Lys 1610	aaa Lys				tat Tyr 1615	gca Ala	-	5712

"The first field with the first first first first first from the first f

cgt Arg	tct Ser	gaa Glu 1620	atc Ile	aga Arg	gga Gly	gtg Val	gat Asp 1625	att Ile	gac Asp	aat Asn	cca Pro	tac Tyr 1630	tct Phe	aac Asn	5757
		acg Thr 1635	gca Ala	ttt Phe	aca Thr	gtc Val	cct Pro 1640					gtt Val 1645		gtg Val	5802
ata Ile	gac Asp	ttc Phe 1650	gat Asp	gca Ala	tct Ser	gag Glu	gaa Glu 1655	cgt Arg	tta Leu	tac Tyr	tgg Trp	aca Thr 1660	gat Asp	att Ile	5847
	aca Thr	caa Gln 1665	acc Thr	att Ile	aaa Lys	cga Arg	gct Ala 1670	ttt Phe	att Ile	aac Asn	gga Gly	act Thr 1675	Gſ ⁷ 333	tta Leu	5892
gaa Glu	act Thr	gtt Val 1680					atr Ile 1685					1690 Gly 999			5937
gtg Val	gat Asp	tgg Trp 1695	gtg Val	tca Ser	cgt Arg	aat Asn	tta Leu 1700					tca Ser 1705			5982
gat Asp	gaa Glu	acg Thr 1710	caa Gln	att Ile	aat Asn	gtg Val	gca Ala 1715	agg A.rg	cta Leu	gat Asp	ggc Gly	tct Ser 1720	ttg Leu	aaa Lys	6027
		att Ile 1725	atc Ile	cat His	gga Gly	atc Ile	gat Asp 1730					ctt Leu 1735			6072
	cca Pro	gtc Val 1740	agg Arg	gga Gly	aaa Lys	ctc Leu	tac Tyr 1745					aac Asn 1750			6117
	atg Met						agt Ser 1760					ctg Leu 1765		cag Gln	6162
		aag Lys 1770	gag Glu	cca Pro	gtt Val	ggt Gly	cta Leu 1775					gtg Val 1780			6207
aag Lys	ctt Leu	tat Tyr 1785	tgg Trp	atc Ile	agt Ser	tog Ser	999 Gly 1790	aat Asn	gga Gly	acc Thr	ata Ile	aat Asn 1795	aga Arg	tgc Cys	6252
		gat Asp 1800	ggt Gly	ggt Gly	aat Asn	tia Leu	gaa Glu 1805	gta Val	atc Ile	gag Glu	tca Ser	atg Met 1810	aaa Lys	gaa Glu	6297
	tta Leu	aca Thr 1815	aaa Lys	gct Ala	aca Thr	gcc Ala	cta Leu 1820	acc Thr	atc Ile	atg Met	gat Asp	aag Lys 1825	aaa Lys	ctg Leu	6342
tgg Trp	tgg Trp	gca Ala 1830	gac Asp	caa Gln	aac Asn	tta Leu	gcc Ala 1835	cag Gln	cta Leu	gga Gly	acc Thr	tgc Cys 1840	agc Ser		6387
	gac Asp	gga Gly 1845	aga Arg	aac Asn	ccc Pro	acc Thr	atc Ile 1850					act Thr 1855	tct Ser		6432

and the stand of t

			cat His 1860					gat Asp 1865								6477
	aat Asn	tcc Ser	tgc Cys 1875	caa Gln	cta Leu	aac Asn	aat Asn	ggt Gly 1880	gga Gly	tgc Cys	tct Ser	caa Cln	ctt ⊔eu 1885	tgt Cys	tta Leu	6522
			tct Ser 1890	gaa Glu	act Thr	aca Thr	agg Arg	act Thr 1895	tgt Cys	atg Met	tgt Cys	aca Thr	gtg Val 1900	gga Gly	tat Tyr	6567
•••			caa Gln 1905	aag Lvs	aac Asn	cgt Arg	atg Met	tca Ser 1910	tgt Cys	caa Gln	ggt Gly	əta Ile	gaa Glu 1915	tca Ser	ttt Phe	6612
, ·			tac Tyr 1920	tct Ser	gtt Val	cat His	gaa Glu	gga Gly 1925	atc Ile	agg Arg	gga Gly	ata Ile	cct Pro 1930	ctt Leu	gaa Glu	6657
٠.	cca Pro	agt Ser	gac Asp 1935	aaa Lys	atg Met	gat Asp	gct Ala	ttg Leu 1940	atg Met	cct Pro	ata Ile	tca Ser	gga Gly 1945	act Thr	tca Ser	6702
	ttt Phe	gcc Ala	gtg Val 1950	gga Gly	ata Ile	gat Asp	ttc Phe	cat His 1955	gca Ala	gaa Glu	aət Asn	gat Asp	acc Thr 1960	atc Ile		6747
	tgg Trp	aca Thr	gac Asp 1965	atg Met	ggc Gly	ttc Phe	aat Asn	aaa Lys 1970	att Ile	agc Ser	aga Arg	gct Ala	aaa Lys 1975	aga Arg	gat Asp	6792
	cag Gln	act Thr	tgg Trp 1980	aaa Lys	gaa Glu	gat Asp	atc Ile	att Ile 1985	acc Thr	aat Asn	ggc Gly	ttg Leu	gga Gly 1990	aga Arg	gtg Val	683"
	gaa Glu	gly ggg	ata Ile 1995	gct Ala	gtt Val	gac Asp	tgg Trp	att Ile 2000	gct Ala	ggt Gly	aac Asn	ata Ile	tat Tyr 2005	tgg Trp	_	6882
•	gat Asp	cat His	ggt Gly 2010	ttc Phe	aac Asn	tta Leu	att Ile	gaa Glu 2015	gtt Val	gca Ala	aga Arg	ctc Leu	aat Asn 2020	ggt Gly		6927
	ttc Phe	cgt Arg	tat Tyr 2025	gta Val	att Ile	att Ile	tcc Ser	caa Gln 2030	ggc Gly	ctg Leu	gat Asp	caa Gln	cca Pro 2035	aga Arg	tct Ser	6972
	ata Ile	gct Ala	gtg Val 2040	cac His	cca Pro	gag Glu	aaa Lys	ggc Gly 2045	ctc Leu	ttg Leu	ttc Phe	tgg Trp	act Thr 2050	gaa Glu	tgg Trp	7017
	gga Gly	caa Gln	atg Met 2055	ccc Pro	tgt Cys	att Ile	gga Gly	aag Lys 2060	gct Ala	cgc Arg	ttg Leu	gat Asp	ggc Gly 2065	tca Ser	gag Glu	7062
	aag Lys	gtt Val	gtc Val 2070	ctt Leu	gta Val	agc Ser	atg Met	gga Gly 2075	ata Ile	gca Ala	tgg Trp	ccg Pro	aat Asn 2080	ggc Gly		7107
	tcc Ser	atc Ile	gac Asp 2085	tat Tyr	gag Glu	gaa Glu	aat Asn	aaa Lys 2090	ttg Leu	tac Tyr	tgg Trp	tgt Cys	gat Asp 2095	gct Ala	cgc Arg	7152

And the first control of the f

			aag Lys 2100	ata Ile	gag Glu	aga Arg	atc Ile	gac Asp 2105	ctt Leu	gag Glu	act Thr	gga Gly	ggg Gly 2110		cgc Arg	ŕ	7197
			gtg Val 2115										tca Ser 2125		gca Ala	-	7242
2.	gtc Val	ttt Phe	ggg Gly 2130	gct Ala	tac Tyr	atc Ile	tac Tyr	tgg Trp 2135	tct Ser	gac Asp	aga Arg	gca Ala	cat His 2140	gca Ala	aac Asn	•	7287
и Мих	gly ggg	tct Ser	gtc Val 2145	aga Arg	agg Arg	ggc Gly	cac His	aag Lys 2150	aat Asn	gat Asp	gcc Ala	aca Thr	gaa Glu 2155		ata Ile	5	7332
	acc Thr	atg Met	aga Arg 2160	acc Thr	ggc Gly	ctt Leu	gga Gly	gtc Val 2165	aac Asn	ctg Leu	aag Lys	gag Glu	gtt Val 2170		ata Ile		7377
Mar a. The second	ttt Phe	aac Asn	cga Arg 2175	gta Val	aga Arg	gag Giu	aaa Lys	999 Gly 2180	acc Thr	aat Asn	gtt Val	tgt Cys	gcc Ala 2185	agg Arg	gac Asp	7	7422
	aat Asn	ggt Gly	ggc Gly 2190	tgt Cys	aag Lys	cəa Gln	ctc Leu	tgt C _y s 2195	ctt Leu	tat Tyr	cga Arg	gga Gly	aat Asn 2200		cgg Arg	7	7467
			tgt Cys 2205	gct Ala	tgt Cys	gcc Ala	cat His	gga Gly 2210	tat Tyr	ttg Leu	gca Ala	gaa Glu	gat Asp 2215	gga Gly	_	7	7512
	act Thr	tgc Cys	ctg Leu 2220	agg Arg	cat His	gaa Glu	gly ggc	tat Tyr 2225	tta Leu	ctg Leu	tat Tyr	tca Ser	gga Gly 2230	aga Arg	aca Thr	7.	7557
	ata Ile	tta Leu	aaa Lys 2235	agt Ser	ata Ile	cat His	ctt Leu	tct Ser 2240	gat Asp	gaa Glu	acc Thr	aat Asn	tta Leu 2245	aat Asr		7	7602
	cca Pro	ata Ile	agg Arg 2250	cca Pro	tat Tyr	gag Glu	aat Asn	cca Pro 2255	cgt Arg	tat Tyr	ttc Phe	aag Lys	aət Asn 2260	gtc Val		7	7647
	gcc Ala	ttg Leu	gct Ala 2265	ttt Phe	gac Asp	tat Tyr	aat Asn	caa Gln 2270	aga Arg	aga Arg	aaa Lys	ggt Gly	acc Thr 2275	aac Asn	cga Arg	7	1692
		ttt Phe	tac Tyr 2280	agt Ser	gat Asp	gca Ala	cac His	ttt Phe 2285	gga Gly	aat Asn	ata Ile	cag Gln	crt Leu 2290	att Ile		7	7737
1		aac Asn	tgg Trp 2295	gaa Glu	gac Asp	aga Arg	caa Gln	gta Val 2300	att Ile	gtt Val	gaa Glu	aat Asn	gtg Val 2305	ggt Gly		7	7782
	gtg Val	gaa Glu	gga Gly 2310	ctt Leu	gcc Ala	tat Tyr	cac His	aga Arg 2315	gcc Ala	tgg Trp	gat Asp	aca Thr	ctg Leu 2320	tac Tyr		7	827
		agc Ser		acc Thr	acc Thr	tca Ser	tcc Ser	atc Ile 2330					gtg Val 2335	gac Asp		7	872

							agg Arg 2345								7917
							cta Leu 2360							aat Asn	7962
	atg Met						aat Asn 2375	_				_		atg Met	8007
_	tct Ser						aat Asn 2390								8052
		ctc Leu 2400					ctt Leu 2405					cgt Arg 2410			8097
	_				_		agt Ser 2420					-		_	8142
							cat His 2435								8187
							gtt Val 2450		_			ata Ile 2455		tgg Trp	8232
_	gac Asp						ata Ile 2465					aag Lys 2470		aca Thr	8277
_		gat Asp 2475					cgt Arg 2480		_			cat His 2485	_		8322
							aat Asn 2495								8367
tct Ser	cca Pro	tgt Cys 2505	gca Ala	tta Leu	ttg Leu	aat Asn	gga Gly 2510	ggc Gly	tgc Cys	cat His	gac Asp	ttg Leu 2515	tgc Cys	ctt Leu	8412
	act Thr		aat Asn	Gly 999	aga Arg	gtg Val	aat Asn 2525	tgt Cys	tcc Ser	tgc Cys	aga Arg	999 91y 2530	gac Asp	cga Arg	8457
	ttg Leu						tgt Cys 2540					tcc Ser 2545			8502
		tat Tyr 2550	tcg Ser	gag Glu	ttt Phe	gaa Glu	tgt Cys 2555	gga Gly				tgc Cys 2560			8547
	cag Gln		acc Thr	tgt Cys	gat Asp	ggc Gly	att Ile 2570					gat Asp 2575			8592

		gat Asp	gaa Glu	aaa Lys 2580	ctg Leu	ctc Leu	tac Tyr	tgt Cys	gaa Glu 2585					cga Arg 2590		ggc Gly		8637
				cca Pro 2595	tgc Cys	tat Tyr	aat Asn	cgc Arg	cgc Arg 2600	tgc Cys	att Ile	cct Pro	cat His	ggc Gly 2605	_	tta Leu		8682
2		tgt Cys	gat Asp	gga Gly 2610	gaa Glu	aat Asn	gac Asp	tgc Cys	gga Gly 2615	gac Asp	aac Asn	tct Ser	gat Asp	gaa Glu 2620	tta Leu	gat Asp	,	8727
* *		tgt Cys	aaa Lys	gtt Val 2625	tca Ser	acc Thr	tgt Cys	gcc Ala	acg Thr 2630	gtt Val	gag Glu	ttc Phe	cgc Arg	tgt Cys 2635	_	gat Asp		8772
		gly aaa	act Thr	tgt Cys 2640	att Ile	cca Pro	aga Arg	tca Ser	gca Ala 2645	cga Arg	tgc Cys	aac Asn	cag Gln	aac Asn 2650	ata Ile	gat Asp		8817
200 A		tgt Cys	gca Ala	gat Asp 2655	gct Ala	tca Ser	gat Asp	gaa Glu	aag Lys 2660	aac Asn	tgc Cys	aat Asn	aac Asn	aca . Thr 2665	gac Asp			8862
Man Ann Man		aca Thr	cat His	ttc Phe 2670	tat Tyr	aag Lys	ctt Leu	gga Gly	gtg Val 2675	aaa Lys	acc Thr	aca Thr	Glà aaa	ttc Phe 2680		aga Arg		8907
Mary Mary Mary		tgt Cys	aat Asn	tct Ser 2685	acc Thr	tca Ser	ctg Leu	tgt Cys	gtt Val 2690					ata Ile 2695	tgc Cys			8952
		Gly aaa	tct Ser	aat Asn 2700	gac Asp	tgt Cys	gga Gly	gac Asp	tat Tyr 2705	tca Ser	gat Asp	gaa Glu	tta Leu	aag Lys 2710	tgc Cys	cca Pro		8997
And the second s									gaa Glu 2720	_				agt Ser 2725	tgt Cys			9042
	-	agt Ser	gga Gly	aga Arg 2730	tgc Cys	att Ile	ttg Leu	aat Asn	acc Thr 2735	tgg Trp	ata Ile	tgc Cys	gat Asp	ggt Gly 2740	cag Gln			9087
									gaa Glu 2750	ttc Phe	cac His	tgt Cys	gat Asp	tct Ser 2755	tot Ser	-		9132
			tgg Trp	aac Asn 2760	caa Gln	ttt Phe	gct Ala	tgt Cys	tcc Ser 2765	gca Ala	caa Gln	aaa Lys	tgt Cys	att Ile 2770	tct Ser	_		9177
.*		cat His	tgg Trp	att Ile 2775	tgt Cys	gat Asp	gga Gly	gaa Glu	gat Asp 2780	gac Asp	tgt Cys	gly aaa	gat Asp	999 Gly 2785	tta Leu			9222
:		Glu	Ser	Asp 2790	Ser	Ile	Cys	Gly	gcc Ala 2795	Tle	Thr	Cys	Ala	Ala 2800	gac Asp			9267
		ttc Phe	agc Ser	tgc Cys 2805	cag Gln	ggc Gly	tct Ser	cgt Arg	gcc Ala 2810	tgc Cys	gtg Val	ccc Pro	cga Arg	cat His 2815	tgg Trp			9312

												gag Glu 2830				9357
												aat Asn 2845				9402
												gtt Val 2860		gac Asp		9447
												ccg Pro 2875				9492
												gct Ala 2890			,	9537
												gac Asp 2905				9582
												aag Lys 2920		aaa Lys		9627
												tgc Cys 2935				9672
												aag Lys 2950	gat Asp	gac Asp		9717
												aat Asn 2965		tgt Cys		9762
ttg Leu	agt Ser	aag Lys 2970	aaa Lys	gtc Val	agt Ser	gga Gly	tgt Cys 2975	tct Ser	caa Gln	gat Asp	tgt Cys	caa Gln 2980	gac Asp	ctt Leu		9807
ccg Pro	gtc Val	agt Ser 2985	tat Tyr	aag Lys	tgc Cys	aaa Lys	tgc Cys 2990	tgg Trp	cct Pro	gga Gly	ttc Phe	caa Gln 2995	ctg Leu	aag Lys		9852
gat Asp	gac Asp	ggc 3000	aaa Lys	aca Thr	tgt Cys	gta Val	gac Asp 3005					tct Ser 3010		ggc Gly		9897
		tgt Cys 3015							aca Thr	tac Tyr	gjà aaa	act Thr 3025	tac Tyr	aag Lys		9942
		tgt Cys 3030	aca Thr	gat Asp	gly ggg	tat Tyr	gaa Glu 3035	ata Ile				aac Asn 3040		aat Asn		9987
	tgc Cys											att Ile 3055			1	.0032

denny party party

			cat His 3060					att Ile 3065								10077
-	aca Thr	ctt Leu	tta Leu 3075	ааа ьуѕ	cag Gln	gga Gly	tta Leu	aac Asn 3980	aat Asn	gtt Val	att Ile	gct Ala	ata Ile 3085	_	ttt Phe	10122
; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;								tat Tyr 3095					agc Ser 3100	cga Arg		10167
• •	aat Asn	ggc Gly	agt Ser 3105	cgc Arg	ata Ile	aat Asn	aga Arg	atg Met 3110	tgt Cys	tta Leu	aat Asn	gga Gly	agt Ser 3115	_	att Ile	10212
¥*	aag Lys	gta Val	gtt Val 3120	cat His	aac Asn	aca Thr	gcg Ala	gtc Val 3125	ccc Pro	aat Asn	gca Ala	ctt Leu	gct Ala 3130	gtc Val	gat Asp	10257
The state of the s								tgg Trp 3140							atc . Ile	10302
and triple pros			gta Val 3150					ggc Gly 3155						ctc Leu	_	10347
Control of the contro			agg Arg 3165					aga Arg 3170							caa Gln	10392
Control of the contro								gac Asp 3185						cat His		10437
A CONTRACTOR OF THE CONTRACTOR			gtt Val 3195					acc Thr 3200					gtc Val 3205		gaa Glu	10482
13 °			att Ile 3210	tct Ser	aga Arg	cct Pro	atg Met	gca Ala 3215	cta Leu	aca Thr	ata Ile	gat Asp	tat Tyr 3220	gtt Val		10527
*	cgt Arg	aga Arg	ctc Leu 3225	tac Tyr	tgg Trp	gcc Ala	gat Asp	gaa Glu 3230	aat Asn	cac His	att Ile	gaa Glu	ttt Phe 3235	agc Ser	aac Asn	10572
	atg Met	gat Asp	gga Gly 3240	tct Ser	cat His	aga Arg	cac His	aaa Lys 3245	gtc Val	cct Pro	aat Asn	caa Gln	gat Asp 3250	att. Ile		10617
a. Ve	gly ggg	gtg Val	att Ile 3255	gca Ala	cta Leu	aca Thr	ttg Leu	ttt Phe 3260					tac Tyr 3265	tgg Irp		19662
·			aaa Lys 3270					agc Ser 3275					aca Thr 3280	tcg Ser		10707
		gac Asp	aga Arg 3285	ctc Leu	tca Ser	ctg Leu	att Ile	tac Tyr 3290			cat His		atc Ile 3295	aca Thr	_	10752

	atc Ile	cag Gln	gtg Val 3300	tat Tyr	cat His	tct Ser	tat Tyr	aga Arg 3305	caa Gln	cct Pro	gat Asp	gtc Val	tcc Ser 3310		cat His	10797
	ctc Leu	tgc Cys	atg Met 3315	ata lle	aat Asn	aat Asn	ggt Gly	ggt Gly 3320	tgc Cys	agt Ser	cat His	ttg Leu	tgc Cys 3325		tta Leu	10842
*	gcc Ala	cct Pro	gga Gly 3330	aaa Lys	acc Thr	cac His	act Thr	tgt Cys 3335	gca Ala	tgt Cys	ccc Pro	act Thr	aac Asn 3340		tat Tyr	10887
	ctg Leu	gca Ala	gct Ala 3345	gat Asp	aat Asn	agg Arg	act Thr	tgc Cys 3350	tta Leu	tcc Ser	aac Asn	tgc Cys	aca Thr 3355	-	agc Ser	10932
	cag Gln	ttt Phe	cgt Arg 3360	cys Cys	aaa Lys	act Thr	gac Asp	aaa Lys 3365	tgt Cys	att Ile	cca Pro	ttc Phe	tgg Trp 3370		aaa Lys	10977
Total	tgt Cys	gac Asp	acc Thr 3375	gtg Val	gat Asp	gac Asp	tgt Cys	ggt Gly 3380	gat Asp	gga Gly	tct Ser	gat Asp	gaa Glu 3385		gat Asp	11022
The state of the s	gac Asp	tgt Cys	cct Pro 3390	gaa Glu	ttt Phe	aga Arg	tgt Cys	cag Gln 3395	cca Pro	ggc Gly	cga Arg	ttt Phe	cag Gln 3400		glà aaa	11067
The first test test test test test	act Thr	gga Gly	ctc Leu 3405	tgt Cys	gct Ala	cta Leu	cca Pro	gct Ala 3410	ttc Phe	atc Ile	tgt Cys	gat Asp	gga Gly 3415	gag Glu		11112
TO THE PARTY OF TH	gat Asp	tgt Cys	gga Gly 3420	gac Asp	aat Asn	tct Ser	gat Asp	gaa Glu 3425					aca Thr 3430	cat His	_	11157
	tga Cys	ctg Leu	tca Ser 3435	ggt Gly	caa Gln	ttc Phe	aaa Lys	tgt Cys 3440					aaa Lys 3445	tgt Cys	atc Ile	11202
			aac Asn 3450	tta Leu	aga Arg	tgt Cys	aat Asn	999 Gly 3455	caa Gln	gat Asp	gac Asp	tgt Cys	ggt Gly 3460	gat Asp		11247
*	gaa Glu	gat Asp	gaa Glu 3465	aga Arg	gac Asp	tgt Cys	cct Pro	gaa Glu 3470	aac Asn	agc Ser	tgt Cys	tct Ser	cca Pro 3475	gac Asp		11292
	ttc Phe	cag Gln	tgt Cys 3480	aag Lys	act Thr	acg Thr	aag Lys	cat His 3485	tgc Cys	att Ile	tcc Ser	aag Lys	ctg Leu 3490	tgg Trp		11337
	tgt Cys	gac Asp	gag Glu 3495	gat Asp	cca Pro	gac Asp	tgt Cys	gca Ala 3500	gat Asp	gca Ala	tca Ser	gac Asp	gag Glu 3505	gcc Ala		11382
	tgc Cys	gat Asp	aaa Lys 3510	aag Lys	act Thr	tgt Cys	gga Gly	cct Pro 3515	cat His	gaa Glu	ttc Phe	cag Gln	tgt Cys 3520	aaa Lys		11427
			tgt Cys 3525	att Ile	ccc Pro	gat Asp	cac His	tgg Trp 3530	cgg Arg	tgt Cys	gat Asp	agc Ser	caa Gln 3535	aat Asn	-	11472

tgc agt gat aat tca gat gaa gaa aac tgt aag cca cag aca tgt
Cys Ser Asp Asn Ser Asp Glu Glu Asn Cys Lys Pro Gln Thr Cys
3540 3545 3550

	aca Thr	ttg Leu	aaa Lys 3555	Asp	ttc Phe	ctc Leu	tgt Cys	gcc Ala 3560	Asn	Gly aaa	gac Asp	tgt Cys	gtt Val 3565		tca Ser	11562
	agg Arg	ttt Phe	tgg Trp 3570	Cys	gat Asp	gga Gly	gat Asp	ttt Phe 3575	Asp	tgt Cys	gca Ala	gat Asp	ggc Gly 3580		gat Asp	11607
	gag Glu	aga Arg	aat Asn 3585	tgt Cys	gag Glu	aca Thr	agt Ser	tgt Cys 3590	tcc Ser	aaa Lys	gat Asp	cag Gln	ttc Phe 3595	cgg Arg	tgt Cys	11652
	tcc Ser	aat Asn	ggt Gly 3600	cag Gln	tgt Cys	ata Ile	cca Pro	gca Ala 3605					gat Asp 3610		cat His	11697
dina denta	gaa Glu	gac Asp	tgc Cys 3615	aaa Lys	tat Tyr	gly 999	gaa Glu	gat Asp 3620	gag Glu	aaa Lys	agc Ser	tgt Cys	gag Glu 3625	cca Pro	gct Ala	11742
Charle Speed Speed	tct Ser	cct Pro	act Thr 3630	tgc Cys	tca Ser	tca Ser	cgt Arg	gaa Glu 3635	tat Tyr	ata Ile	tgt Cys	gcc Ala	agt Ser 3640	gat Asp	gga Gly	11787
Soul Soul of the	tgt Cys	att Ile	tca Ser 3645	gca Ala	tct Ser	ttg Leu	aaa Lys	tgt Cys 3650	aat Asn	gga Gly	gaa Glu	tat Tyr	gat Asp 3655	tgt Cys	gct Ala	11832
	gat Asp	ggt Gly	tca Ser 3660	gat Asp	gag Glu	atg Met	gac Asp	tgt Cys 3665	gtg Val	act Thr	gaa Glu	tgt Cys	aag Lys 3670		gat Asp	11877
Company of the state of the sta	cag Gln	ttt Phe	cgg Arg 3675	tgc Cys	aaa Lys	aat Asn	aaa Lys	gcc Ala 3680	cac His	tgt Cys	att Ile	cca Pro	att Ile 3685	aga Arg	tgg Trp	11922
	ctg Leu	tgt Cys	gat Asp 3690	gga Gly	att Ile	cat His	gac Asp	tgt Cys 3695	gtg Val	gat Asp	ggc Gly	agt Ser	gat Asp 3700		gag Glu	11967
	aac Asn	tgt Cys	gaa Glu 3705	aga Arg	gga Gly	gga Gly	aat Asn	ata Ile 3710	tgt Cys	aga Arg	gct Ala	gat Asp	gag Glu 3715	ttc Phe		12012
	tgc Cys	aat Asn	aat Asn 3720	tct Ser	ctc Leu	tgc Cys	aaa Lys	cta Leu 3725	cat His	ttc Phe	tgg Trp	gtg Val	tgt Cys 3730	gat Asp		12057
	gag Glu	gac Asp	gac Asp 3735	tgt Cys	gga Gly	gac Asp	aac Asn	tct Ser 3740	gat Asp	gaa Glu	gcc Ala	cct Pro	gat Asp 3745	atg Met	tgt Cys	12102
	gtc Val	aaa Lys	ttt Phe 3750	ctt Leu	tgt Cys	cca Pro	tcc Ser	acg Thr 3755	aga Arg	cct Pro	cac His	aga Arg	tgc Cys 3760	aga Arg	aat Asn	12147
	aac Asn	aga Arg	ata Ile 3765	tgc Cys	cta Leu	cag Gln	tcg Ser	gag Glu 3770	caa Gln	atg Met	tgc Cys	aat Asn	ggg Gly 3775	att Ile	_	12192

					gaa Glu 3785					12237
					aaa Lys 3800					12282
	aaa Lys				gat Asp 3815					12327
					gag Glu 3830					12372
					aat Asn 3845				gat Asp	12417
_		_			aca Thr 3860			cgc Arg 3865		12462
					aaa Lys 3875			gaa Glu 3880	ctt Leu	12507
					aca Thr 3890					12552
					gtg Val 3905				gaa Glu	12597
_		aac Asn 3915			gaa Glu 3920				ctc Leu	12642
					atc Ile 3935					12687
					caa Gln 3950					12732
	aga Arg	ata Ile 3960			gta Val 3965					12777
	tgg Trp				cca Pro 3980					12822
	cat His				caa Gln 3995			ttg Leu 4000	tgt Cys	12867
cct Pro	gaa	_			gac Asp			tgg Trp		12912

_		att Ile 4020					cat His 4025					tgg Trp 4030			12957
		act Thr 4035					agt Ser 4040					atc Ile 4045	aac Asn		13002
		ctg Leu 4050					tgc Cys 4055						aat Asn	_	13047
_		gaa Glu 4065					gca Ala 4070								13092
_		tgg Trp 4080					gat Asp 4085							_	13137
							agg Arg 4100					aag Lys 4105		tta Leu	13182
		ccc Pro 4110			_	_	gtg Val 4115	_			_	gaa Glu 4120	_		13227
							tcc Ser 4130						ctg Leu		13272
		tct Ser 4140					tct Ser 4145					caa Gln 4150			13317
		cca Pro 4155	cat His	agg Arg	atc Ile	gat Asp	atc Ile 4160					ata Ile 4165		gga Gly	13362
		Pro					ttt	cqa	att						13407
		4170	•	73011	GIÀ	Val	Phe 4175					ttt Phe 4180			13107
	tca Ser	gta	gag	tac	tta	gct		Arg	Val	Gln gat	Lys aaa	Phe 4180 aca	Gly	His ggt	13452
Gly gtt		gta Val 4185 ata	gag Glu tct	tac Tyr cat	tta Leu cgt	gct Ala tat	4175 tta Leu	Arg aat Asn	Val att Ile cta	Gln gat Asp gat	Lys aaa Lys tta	Phe 4180 aca Thr 4195	Gly aaa Lys	His ggt Gly cca	
gtt Val tgc	ser ttg Leu ttg	gta Val 4185 ata Ile 4200 gat	gag Glu tct Ser	tac Tyr cat His	tta Leu cgt Arg	gct Ala tat Tyr	tta Leu 4190 aaa Lys	Arg aat Asn caa Gln ctt	Val att Ile cta Leu tgc	Gln gat Asp gat Asp	Lys aaa Lys tta Leu cta	Phe 4180 aca Thr 4195 ccc Pro 4210 aat	Gly aaa Lys aat Asn	His ggt Gly cca Pro	13452
gtt Val tgc Cys	Ser ttg Leu ttg Leu	gta Val 4185 ata Ile 4200 gat Asp 4215 act	gag Glu tct Ser tta Leu	tac Tyr cat His gca Ala	tta Leu cgt Arg tgc Cys	gct Ala tat Tyr gaa Glu	tta Leu 4190 aaa Lys 4205 ttt Phe	aat Asn caa Gln ctt Leu	Val att Ile cta Leu tgc Cys	Gln gat Asp gat Asp ttg Leu tat	Lys aaa Lys tta Leu cta Leu	Phe 4180 aca Thr 4195 ccc Pro 4210 aat Asn 4225 att	Gly aaa Lys aat Asn	His ggt Gly cca Pro tct Ser	13452 13497

_	_				_	-	att Ile 4265					-	_	13677
	-		_			_	tat Tyr 4280				tgt Cys 4285		_	13722
		-	_			_	cag Gln 4295				tgc Cys 4300		cca Pro	13767
							tgc Cys 4310							13812
							gtc Val 4325						aat Asn	13857
							gct Ala 4340							13902
							gac Asp 4355							13947
							gaa Glu 4370							13992
							cca Pro 4385	_			gga Gly 4390			14037
							agg Arg 4400				cac His 4405		att Ile	14082
_			_	_	_	_	ata Ile 4415		_	_	act Thr 4420			14127
		gcc Ala 4425					tta Leu 4430							14172
							ccc Pro 4445							14217
	tgc Cys	tcc Ser 4455					ggc Gly 4460				agg Arg 4465			14262
	aag Lys	agc Ser 4470		_			cat His 4475		_	_	agc Ser 4480		gcc Ala	14307
_	_	gtg Val 4485					ttg Leu 4490							14352

gta att ggt tta gtg ctt tgt aaa aga aaa aga agg aca aaa aca Val Ile Gly Leu Val Leu Cys Lys Arg Lys Arg Arg Thr Lys Thr 4500 4505 4510	14397
att aga aga caa cct att atc aat gga gga ata aat gta gaa att Ile Arg Arg Gln Pro Ile Ile Asn Gly Gly Ile Asn Val Glu Ile 4515 4520 4525	14442
ggc aat cca tct tat aac atg tat gag gta gat cat gat cac aac Gly Asn Pro Ser Tyr Asn Met Tyr Glu Val Asp His Asp His Asn 4530 4535 4540	14487
gat gga ggt ctt tta gat cct ggc ttt atg ata gac cca aca aag Asp Gly Gly Leu Leu Asp Pro Gly Phe Met Ile Asp Pro Thr Lys 4545 4550 4555	14532
gcc agg tac ata ggg gga gga ccc agt gct ttc aag ctt cca cac Ala Arg Tyr Ile Gly Gly Pro Ser Ala Phe Lys Leu Pro His 4560 4565 4570	14577
aca gcg ccg ccc atc tac cta aac tct gat ttg aaa gga cca cta Thr Ala Pro Pro Ile Tyr Leu Asn Ser Asp Leu Lys Gly Pro Leu 4575 4580 4585	14622
act gct ggg cca aca aat tac tcc aat ccg gta tat gca aaa tta Thr Ala Gly Pro Thr Asn Tyr Ser Asn Pro Val Tyr Ala Lys Leu 4590 4595 4600	14667
tat atg gat ggg caa aac tgt cga aac tcc tta gga agt gtt gat Tyr Met Asp Gly Gln Asn Cys Arg Asn Ser Leu Gly Ser Val Asp 4605 4610 4615	14712
gaa agg aaa gaa ctg ctt cca aag aaa ata gaa att ggt ata aga Glu Arg Lys Glu Leu Leu Pro Lys Lys Ile Glu Ile Gly Ile Arg 4620 4625 4630	14757
gag aca gtg gca taatcagtga tatcttttat atgctgtata aatgtataag Glu Thr Val Ala 4635	14809
aatattagga gtacatttgg tatgtcccaa caggtattat acgtggttgg catcagcatt	14869
acctctttct ttatcttttt cctggttaat tgttttctga gttttttggg ttttattttt	14929
tgctgatgac tattgattga ccatttgtat ggtattttta tgaaaaagaa ctgcactaca	14989
gtacaattta caacaatgct gctgatatga cacacctttg aatttgttaa aattaaaaac	15049
aacgtattcc tttgtagtgt gaatatgagc aatctatttt atatgaactt ttttggttgt	15109
acttaatcaa cgaggagaat ctctgcactt ttccattata cggtttgaag gctgtaatac	15169
agtgtcattt tatttttctg tttaaattga tggaaaaatg attgaatggt caactctctt	15229
ctttgtgccc ataaagatcg attcagactc tgctgaaaat atatagctct cacaagttca	15289
gcatcacctg ctttgaaatt agccttagat tgccaaccaa tagatgagaa ttttgaggaa	15349
aaaaattaaa aatatgtaaa attaataatt tgcatgaaca cagatgacta cattttccaa	15409
aacttagtgg actctatgtg atgtactaaa tgtatacacc ttgtaagcaa tagttatatt	15469
taggtggtag aacatagcaa aaatataacc gaaagttggc cgactgcact tgctatggaa	15529

taaqaccttt tattctccct caqtctcqaq ataaatagcc agcctagagc acaacagggc 15589 attgggtact tgcatcttag gtatttcttc ccagtcacat ccattttgtg gaagattaac 15649 ccaaccectt acactacact gaacactaaa gaataacata taagcacaca aattggtgac 15709 aqaatttcaa ttacqtqaac gcatcctctt tgctaggtca aaaacaaagg gcaaagcaga 15769 cattttagta tacagagtga ttggcaaata ttttcaagat ttaatatgag caacccatta 15829 tttqccctat ccaaaatata ttcaagggcc ttccaagttg tagaagaaca atgatcttcc 15889 cataatcaaa agtggagagt cgaaatgctg tgccagttgc tctggtattc aggtttctct 15949 gggttttaca gaacgcatgg accccattca cgtttggttt gtttatcttc aaatttgagt 16009 tgaaacgagt gcgatttatt taagttgtat ataaaaataa aaggatagca tttttataca 16069 aatatettta aaggeacaaa agatttatte acaagttttg gagggetttt tgtteetetg 16129 atagacatga ctgactttta gctgtcataa tgtattaacc taacagatga aatatgttaa 16189 atatgtggtt gctctttatc cctttgtaca agcattaaaa aaactgctgt tttataagaa 16249 gactttttgt tgtactatgt gcatgcatac tacctatttc taaactttgc catattgagg 16309 cctttataaa ctattgattt atgtaatact agtgcaattt tgcttgaaca atgttatgca 16369 tatcataaac tttttcaggt tcttgtttaa gtacattttt taaattgaac agtatttttc 16429 attttggtta taatatagtc attttgccta tgtttctaca atgaagtgtt aaatacttta 16489 taaaaaaattq ttqactqact tatttaaatq aaattctaca tatttaaaaa aaaaaa 16545

<210> 33 <211> 4636

<212> PRT

<213> Homo sapiens

<400> 33

Met Thr Pro Leu Gly Ser Arg Leu Gln Ala Ala Pro Ala Ala Ala Ala 1 5 10 15

Ala Ala Gly Pro Lys Val Pro Pro Ser Ser Leu Gln Arg Arg Leu Pro 20 25 30

Tyr Arg Ala Thr Thr Met Ser Glu Phe Leu Leu Ala Leu Leu Thr Leu 35 40 45

Ser Gly Leu Leu Pro Ile Ala Arg Val Leu Thr Val Gly Ala Asp Arg 50 55 60

Asp Gln Gln Leu Cys Asp Pro Gly Glu Phe Leu Cys His Asp His Val 65 70 75 80

Thr Cys Val Ser Arg Ser Trp Leu Cys Asp Gly Asp Pro Asp Cys Pro

Asn Val Gln Gln Met Ala Ile Asp Trp Leu Thr Arg Asn Leu Tyr Phe

Val Asp His Val Gly Asp Arg Ile Phe Val Cys Asn Ser Asn Gly Ser 340 345 350

Val Cys Val Thr Leu Ile Asp Leu Glu Leu His Asn Pro Lys Ala Ile 355 360 365

Ala Val Asp Pro Ile Ala Gly Lys Leu Phe Phe Thr Asp Tyr Gly Asn 370 375 380

Val Ala Lys Val Glu Arg Cys Asp Met Asp Gly Met Asn Arg Thr Arg 385 390 395 400

Ile Ile Asp Ser Lys Thr Glu Gln Pro Ala Ala Leu Ala Leu Asp Leu 405 410 415

Val Asn Lys Leu Val Tyr Trp Val Asp Leu Tyr Leu Asp Tyr Val Gly 420 425 430

Gln Val Arg His Leu Tyr Gly Ile Thr Val Phe Glu Asp Tyr Leu Tyr 450 455 460

Ala Thr Asn Ser Asp Asn Tyr Asn Ile Val Arg Ile Asn Arg Phe Asn 465 470 475 480

Gly Thr Asp Ile His Ser Leu Ile Lys Ile Glu Asn Ala Trp Gly Ile 485 490 495

Arg Ile Tyr Gln Lys Arg Thr Gln Pro Thr Val Arg Ser His Ala Cys $500 \hspace{1.5cm} 505 \hspace{1.5cm} 510$

Glu Val Asp Pro Tyr Gly Met Pro Gly Gly Cys Ser His Ile Cys Leu 515 520 525

Leu Ser Ser Ser Tyr Lys Thr Arg Thr Cys Arg Cys Arg Thr Gly Phe 530 540

Asn Leu Gly Ser Asp Gly Arg Ser Cys Lys Arg Pro Lys Asn Glu Leu 545 550 555 560

Phe Leu Phe Tyr Gly Lys Gly Arg Pro Gly Ile Val Arg Gly Met Asp

Leu Asn Thr Lys Ile Ala Asp Glu Tyr Met Ile Pro Ile Glu Asn Leu 580 585 590

Val Asn Pro Arg Ala Leu Asp Phe His Ala Glu Thr Asn Tyr Ile Tyr 595 600 605

Phe Ala Asp Thr Thr Ser Phe Leu Ile Gly Arg Gln Lys Ile Asp Gly 610 620

Thr Glu Arg Glu Thr Ile Leu Lys Asp Asp Leu Asp Asn Val Glu Gly 625 630 635 640

Ile Ala Val Asp Trp Ile Gly Asn Asn Leu Tyr Trp Thr Asn Asp Gly 645 650 655

His Arg Lys Thr Ile Asn Val Ala Arg Leu Glu Lys Ala Ser Gln Ser 660 665 670

Arg Lys Thr Leu Leu Glu Gly Glu Met Ser His Pro Arg Gly Ile Val 675 680 685

Val Asp Pro Ile Asn Gly Trp Met Tyr Trp Thr Asp Trp Glu Glu Asp 690 695 700

Glu Ile Asp Asp Ser Val Gly Arg Ile Glu Lys Ala Trp Met Asp Gly 705 710 715 720

Phe Asn Arg Gln Ile Phe Val Thr Ser Lys Met Leu Trp Pro Asn Gly 725 730 735

Leu Thr Leu Asp Phe His Thr Asn Thr Leu Tyr Trp Cys Asp Ala Tyr 740 745 750

Tyr Asp His Ile Glu Lys Val Phe Leu Asn Gly Thr His Arg Lys Ile 755 760 765

Val Tyr Ser Gly Arg Glu Leu Asn His Pro Phe Gly Leu Ser His His 770 780

Gly Asn Tyr Val Phe Trp Thr Asp Tyr Met Asn Gly Ser Ile Phe Gln 785 790 795 800

Leu Asp Leu Ile Thr Ser Glu Val Thr Leu Leu Arg His Glu Arg Pro 805 810 815

Pro Leu Phe Gly Leu Gln Ile Tyr Asp Pro Arg Lys Gln Gln Gly Asp 820 825 830

Asn Met Cys Arg Val Asn Asn Gly Gly Cys Ser Thr Leu Cys Leu Ala 835 840 845

- Ile Pro Gly Gly Arg Val Cys Ala Cys Ala Asp Asn Gln Leu Leu Asp 850 860
- Glu Asn Gly Thr Thr Cys Thr Phe Asn Pro Gly Glu Ala Leu Pro His 865 870 875 880
- Ile Cys Lys Ala Gly Glu Phe Arg Cys Lys Asn Arg His Cys Ile Gln 885 890 895
- Ala Arg Trp Lys Cys Asp Gly Asp Asp Asp Cys Leu Asp Gly Ser Asp 900 905 910
- Glu Asp Ser Val Asn Cys Phe Asn His Ser Cys Pro Asp Asp Gln Phe 915 920 925
- Lys Cys Gln Asn Asn Arg Cys Ile Pro Lys Arg Trp Leu Cys Asp Gly 930 940
- Ala Asn Asp Cys Gly Ser Asn Glu Asp Glu Ser Asn Gln Thr Cys Thr 945 950 955 960
- Ala Arg Thr Cys Gln Val Asp Gln Phe Ser Cys Gly Asn Gly Arg Cys 965 970 975
- Ile Pro Arg Ala Trp Leu Cys Asp Arg Glu Asp Asp Cys Gly Asp Gln 980 985 990
- Thr Asp Glu Met Ala Ser Cys Glu Phe Pro Thr Cys Glu Pro Leu Thr 995 1000 1005
- Gln Phe Val Cys Lys Ser Gly Arg Cys Ile Ser Ser Lys Trp His 1010 1015 1020
- Cys Asp Ser Asp Asp Cys Gly Asp Gly Ser Asp Glu Val Gly 1025 1030 1035
- Cys Val His Ser Cys Phe Asp Asn Gln Phe Arg Cys Ser Ser Gly 1040 1045 1050
- Arg Cys Ile Pro Gly His Trp Ala Cys Asp Gly Asp Asn Asp Cys 1055 1060 1065
- Gly Asp Phe Ser Asp Glu Ala Gln Ile Asn Cys Thr Lys Glu Glu 1070 1075 1080
- Ile His Ser Pro Ala Gly Cys Asn Gly Asn Glu Phe Gln Cys His 1085 1090 1095

- Pro Asp Gly Asn Cys Val Pro Asp Leu Trp Arg Cys Asp Gly Glu 1100 $\,$ 1110
- Lys Asp Cys Glu Asp Gly Ser Asp Glu Lys Gly Cys Asn Gly Thr 1115 1120 1125
- Ile Arg Leu Cys Asp His Lys Thr Lys Phe Ser Cys Trp Ser Thr 1130 1140
- Gly Arg Cys Ile Asn Lys Ala Trp Val Cys Asp Gly Asp Ile Asp 1145 1150 1155
- Cys Glu Asp Gln Ser Asp Glu Asp Asp Cys Asp Ser Phe Leu Cys 1160 1165
- Gly Pro Pro Lys His Pro Cys Ala Asn Asp Thr Ser Val Cys Leu 1175 1180 1185
- Gln Pro Glu Lys Leu Cys Asn Gly Lys Lys Asp Cys Pro Asp Gly 1190 1195 1200
- Ser Asp Glu Gly Tyr Leu Cys Asp Glu Cys Ser Leu Asn Asn Gly 1205 1210
- Gly Cys Ser Asn His Cys Ser Val Val Pro Gly Arg Gly Ile Val 1220 1225 1230
- Cys Ser Cys Pro Glu Gly Leu Gln Leu Asn Lys Asp Asn Lys Thr 1235 1240 1245
- Cys Glu Ile Val Asp Tyr Cys Ser Asn His Leu Lys Cys Ser Gln 1250 1260
- Val Cys Glu Gln His Lys His Thr Val Lys Cys Ser Cys Tyr Glu 1265 1270 1275
- Gly Trp Lys Leu Asp Val Asp Gly Glu Ser Cys Thr Ser Val Asp 1280 1285
- Pro Phe Glu Ala Phe Ile Ile Phe Ser Ile Arg His Glu Ile Arg 1295 1300 1305
- Arg Ile Asp Leu His Lys Arg Asp Tyr Ser Leu Leu Val Pro Gly 1310 1320
- Leu Arg Asn Thr Ile Ala Leu Asp Phe His Phe Asn Gln Ser Leu 1325 1330 1335

									_					
Leu	Tyr 1340	Trp	Thr	Asp	Val	Val 1345	Glu	Asp	Arg	Ile	Tyr 1350	Arg	Gly	Lys
Leu	Ser 1355	Glu	Ser	Gly	Gly	Val 1360	Ser	Ala	Ile	Glu	Val 1365	Val	Val	Glu
His	Gly 1370	Leu	Ala	Thr	Pro	Glu 1375	Gly	Leu	Thr	Val	Asp 1380	Trp	Ile	Ala
Gly	Asn 1385	Ile	Tyr	Trp	Ile	Asp 1390		Asn	Leu	Asp	Gln 1395	Ile	Glu	Val
Ala	Lys 1400	Leu	Asp	Gly	Ser	Leu 1405	Arg	Thr	Thr	Leu	Ile 1410	Ala	Gly	Ala
Met	Glu 1415	His	Pro	Arg	Ala	Ile 1420	Ala	Leu	Asp	Pro	Arg 1425	Tyr	Gly	Ile
Leu	Phe 1430	Trp	Thr	Asp	Trp	Asp 1435	Ala	Asn	Phe	Pro	Arg 1440	Ile	Glu	Ser
Ala	Ser 1445	Met	Ser	Gly	Ala	Gly 1450	Arg	Lys	Thr	Ile	Tyr 1455	Lys	Asp	Met
Lys	Thr 1460	_	Ala	Trp	Pro	Asn 1465	Gly	Leu	Thr	Val	Asp 1470		Phe	Glu
Lys	Arg 1475		Val	Trp	Thr	Asp 1480	Ala	Arg	Ser	Asp	Ala 1485	Ile	Tyr	Ser
Ala	Leu 1490	-	Asp	Gly	Thr	Asn 1495		Ile	Glu	Ile	Ile 1500	_	Gly	His
Glu	Tyr 1505		Ser	His	Pro	Phe 1510		Val	Ser	Leu	Tyr 1515		Ser	Glu
Val	Tyr 1520		Thr	Asp	Trp	Arg 1525		Asn	Thr	Leu	Ser 1530		Ala	Asn
Lys	Trp 1535		Gly	Gln	Asn	Val 1540		Val	Ile	Gln	Lys 1545		Ser	Ala
Gln	Pro 1550		Asp	Leu	Gln	Ile 1555		His	Pro	Ser	Arg 1560		Pro	Gln
_														

Ala Pro Asn Pro Cys Ala Ala Asn Asp Gly Lys Gly Pro Cys Ser 1565

- His Met Cys Leu Ile Asn His Asn Arg Ser Ala Ala Cys Ala Cys 1580 1585 1590
- Pro His Leu Met Lys Leu Ser Ser Asp Lys Lys Thr Cys Tyr Glu 1595 1600 1605
- Met Lys Lys Phe Leu Leu Tyr Ala Arg Arg Ser Glu Ile Arg Gly 1610 1620
- Val Asp Ile Asp Asn Pro Tyr Phe Asn Phe Ile Thr Ala Phe Thr 1625 1630 1635
- Val Pro Asp Ile Asp Asp Val Thr Val Ile Asp Phe Asp Ala Ser 1640 1650
- Glu Glu Arg Leu Tyr Trp Thr Asp Ile Lys Thr Gln Thr Ile Lys 1655 1660 1665
- Arg Ala Phe Ile Asn Gly Thr Gly Leu Glu Thr Val Ile Ser Arg 1670 1675 1680
- Asp Ile Gln Ser Ile Arg Gly Leu Ala Val Asp Trp Val Ser Arg 1685 1690 1695
- Asn Leu Tyr Trp Ile Ser Ser Glu Phe Asp Glu Thr Gln Ile Asn 1700 1705 1710
- Val Ala Arg Leu Asp Gly Ser Leu Lys Thr Ser Ile Ile His Gly 1715 1720
- Ile Asp Lys Pro Gln Cys Leu Ala Ala His Pro Val Arg Gly Lys 1730 1735 1740
- Leu Tyr Trp Thr Asp Gly Asn Thr Ile Asn Met Ala Asn Met Asp 1745 1750 1755
- Gly Ser Asn Ser Lys Ile Leu Phe Gln Asn Gln Lys Glu Pro Val 1760 1765 1770
- Gly Leu Ser Ile Asp Tyr Val Glu Asn Lys Leu Tyr Trp Ile Ser 1775 1780 1785
- Ser Gly Asn Gly Thr Ile Asn Arg Cys Asn Leu Asp Gly Gly Asn 1790 1800
- Leu Glu Val Ile Glu Ser Met Lys Glu Glu Leu Thr Lys Ala Thr 1805 1810 1815

Ala Leu Thr Ile Met Asp Lys Lys Leu Trp Trp Ala Asp Gln Asn Leu Ala Gln Leu Gly Thr Cys Ser Lys Arg Asp Gly Arg Asn Pro 1840 1835 Thr Ile Leu Arg Asn Lys Thr Ser Gly Val Val His Met Lys Val 1855 Tyr Asp Lys Glu Ala Gln Gln Gly Ser Asn Ser Cys Gln Leu Asn 1870 1865 Asn Gly Gly Cys Ser Gln Leu Cys Leu Pro Thr Ser Glu Thr Thr 1885 1880 Arg Thr Cys Met Cys Thr Val Gly Tyr Tyr Leu Gln Lys Asn Arg 1895 1900 Met Ser Cys Gln Gly Ile Glu Ser Phe Leu Met Tyr Ser Val His 1910 1915 1920 Glu Gly Ile Arg Gly Ile Pro Leu Glu Pro Ser Asp Lys Met Asp 1935 1925 1930 Ala Leu Met Pro Ile Ser Gly Thr Ser Phe Ala Val Gly Ile Asp 1940 1945 Phe His Ala Glu Asn Asp Thr Ile Tyr Trp Thr Asp Met Gly Phe 1955 1960 Asn Lys Ile Ser Arg Ala Lys Arg Asp Gln Thr Trp Lys Glu Asp 1970 Ile Ile Thr Asn Gly Leu Gly Arg Val Glu Gly Ile Ala Val Asp 1985 1990 1995 Trp Ile Ala Gly Asn Ile Tyr Trp Thr Asp His Gly Phe Asn Leu Ile Glu Val Ala Arg Leu Asn Gly Ser Phe Arg Tyr Val Ile Ile 2015 2020 2025 Ser Gln Gly Leu Asp Gln Pro Arg Ser Ile Ala Val His Pro Glu 2030 2035 2040

Lys Gly Leu Leu Phe Trp Thr Glu Trp Gly Gln Met Pro Cys Ile

2055

2050

									_					
Gly	Lys 2060	Ala	Arg	Leu	Asp	Gly 2065	Ser	Glu	Lys	Val	Val 2070	Leu	Val	Ser
Met	Gly 2075	Ile	Ala	Trp	Pro	Asn 2080	Gly	Ile	Ser	Ile	Asp 2085	Tyr	Glu	Glu
Asn	Lys 2090	Leu	Tyr	Trp	Cys	Asp 2095	Ala	Arg	Thr	Asp	Lys 2100	Ile	Glu	Arg
Ile	Asp 2105	Leu	Glu	Thr	Gly	Gly 2110	Asn	Arg	Glu	Met	Val 2115	Leu	Ser	Gly
Ser	Asn 2120	Val	Asp	Met	Phe	Ser 2125	Val	Ala	Val	Phe	Gly 2130	Ala	Tyr	Ile
Tyr	Trp 2135	Ser	Asp	Arg	Ala	His 2140		Asn	Gly	Ser	Val 2145	Arg	Arg	Gly
His	Lys 2150	Asn	Asp	Ala	Thr	Glu 2155	Thr	Ile	Thr	Met	Arg 2160	Thr	Gly	Leu
Gly	Val 2165	Asn	Leu	Lys	Glu	Val 2170	_	Ile	Phe	Asn	Arg 2175	Val	Arg	Glu
Lys	Gly 2180		Asn	Val	Cys	Ala 2185		Asp	Asn	Gly	Gly 2190	Cys	Lys	Gln
Leu	Cys 2195	Leu	Tyr	Arg	Gly	Asn 2200		Arg	Arg	Thr	Cys 2205	Ala	Cys	Ala
His	Gly 2210	_	Leu	Ala	Glu	Asp 2215	_	Val	Thr	Cys	Leu 2220	Arg	His	Glu
Gly	Tyr 2225		Leu	Tyr	Ser	Gly 2230		Thr	Ile	Leu	Lys 2235		Ile	His
Leu	Ser 2240	-	Glu	Thr	Asn	Leu 2245		Ser	Pro	Ile	Arg 2250	Pro	Tyr	Glu
Asn	Pro 2255	_	Tyr	Phe	Lys	Asn 2260		Ile	Ala	Leu	Ala 2265		Asp	Tyr
Asn	Gln 2270	_	Arg	Lys	Gly	Thr 2275		Arg	Ile	Phe	Tyr 2280		Asp	Ala

His Phe Gly Asn Ile Gln Leu Ile Lys Asp Asn Trp Glu Asp Arg 2285 2290 2295

Gln Val Ile Val Glu Asn Val Gly Ser Val Glu Gly Leu Ala Tyr 2305 His Arg Ala Trp Asp Thr Leu Tyr Trp Thr Ser Ser Thr Thr Ser 2315 2320 Ser Ile Thr Arg His Thr Val Asp Gln Thr Arg Pro Gly Ala Phe 2335 2330 Asp Arg Glu Ala Val Ile Thr Met Ser Glu Asp Asp His Pro His 2345 2350 Val Leu Ala Leu Asp Glu Cys Gln Asn Leu Met Phe Trp Thr Asn 2365 Trp Asn Glu Gln His Pro Ser Ile Met Arg Ser Thr Leu Thr Gly 2380 2385 2375 Lys Asn Ala Gln Val Val Ser Thr Asp Ile Leu Thr Pro Asn 2395 2390 Gly Leu Thr Ile Asp Tyr Arg Ala Glu Lys Leu Tyr Phe Ser Asp 2405 2410 2415 Gly Ser Leu Gly Lys Ile Glu Arg Cys Glu Tyr Asp Gly Ser Gln Arg His Val Ile Val Lys Ser Gly Pro Gly Thr Phe Leu Ser Leu 2435 2440 2445 Ala Val Tyr Asp Asn Tyr Ile Phe Trp Ser Asp Trp Gly Arg Arg 2455 Ala Ile Leu Arg Ser Asn Lys Tyr Thr Gly Gly Asp Thr Lys Ile 2470 Leu Arg Ser Asp Ile Pro His Gln Pro Met Gly Ile Ile Ala Val Ala Asn Asp Thr Asn Ser Cys Glu Leu Ser Pro Cys Ala Leu Leu 2495 2500 2505 Asn Gly Gly Cys His Asp Leu Cys Leu Leu Thr Pro Asn Gly Arg 2510

Val Asn Cys Ser Cys Arg Gly Asp Arg Ile Leu Leu Glu Asp Asn

2535

2530

									,					
Arg	Cys 2540	Val	Thr	Lys	Asn	Ser 2545	Ser	Cys	Asn	Ala	Tyr 2550	Ser	Glu	Phe
Glu	Cys 2555	Gly	Asn	Gly	Glu	Cys 2560	Ile	Asp	Tyr	Gln	Leu 2565	Thr	Cys	Asp
Gly	Ile 2570	Pro	His	Cys	Lys	Asp 2575	Lys	Ser	Asp	Glu	Lys 2580	Leu	Leu	Tyr
Cys	Glu 2585	Asn	Arg	Ser	Cys	Arg 2590	Arg	Gly	Phe	Lys	Pro 2595	Cys	Tyr	Asn
Arg	Arg 2600	Cys	Ile	Pro	His	Gly 2605	Lys	Leu	Cys	Asp	Gly 2610	Glu	Asn	Asp
Cys	Gly 2615	Asp	Asn	Ser	Asp	Glu 2620		Asp	Cys	Lys	Val 2625	Ser	Thr	Cys
Ala	Thr 2630	Val	Glu	Phe	Arg	Cys 2635	Ala	Asp	Gly	Thr	Cys 2640	Ile	Pro	Arg
Ser	Ala 2645	Arg	Cys	Asn	Gln	Asn 2650		Asp	Cys	Ala	Asp 2655		Ser	Asp
Glu	Lys 2660		Cys	Asn	Asn	Thr 2665	_	Cys	Thr	His	Phe 2670		Lys	Leu
Gly	Val 2675	Lys	Thr	Thr	Gly	Phe 2680		Arg	Cys	Asn	Ser 2685		Ser	Leu
Cys	Val 2690	Leu	Pro	Thr	Trp	Ile 2695		Asp	Gly	Ser	Asn 2700		Cys	Gly
Asp	Tyr 2705		Asp	Glu	Leu	Lys 2710		Pro	Val	Gln	Asn 2715		His	Lys
Cys	Glu 2720		Asn	Tyr	Phe	Ser 2725	_	Pro	Ser	Gly	Arg 2730	_	Ile	Leu
Asn	Thr 2735		Ile	Cys	Asp	Gly 2740		Lys	Asp	Суз	Glu 2745		Gly	Arg
Asp	Glu 2750		His	Cys	Asp	Ser 2755		Cys	Ser	Trp	Asn 2760		Phe	Ala

Cys Ser Ala Gln Lys Cys Ile Ser Lys His Trp Ile Cys Asp Gly 2765 2770 2775

Glu	Asp 2780	Asp	Cys	Gly	Asp	Gly 2785	Leu	Asp	Glu	Ser	Asp 2790	Ser	Ile	Cys
Gly	Ala 2795	Ile	Thr	Cys	Ala	Ala 2800	Asp	Met	Phe	Ser	Cys 2805	Gln	Gly	Ser
Arg	Ala 2810	Cys	Val	Pro	Arg	His 2815	Trp	Leu	Cys	Asp	Gly 2820	Glu	Arg	Asp
Cys	Pro 2825	Asp	Gly	Ser	Asp	Glu 2830	Leu	Ser	Thr	Ala	Gly 2835	Cys	Ala	Pro
Asn	Asn 2840	Thr	Cys	Asp	Glu	Asn 2845	Ala	Phe	Met	Cys	His 2850	Asn	Lys	Val
Cys	Ile 2855	Pro	Lys	Gln	Phe	Val 2860	Cys	Asp	His	Asp	Asp 2865	Asp	Cys	Gly
Asp	Gly 2870	Ser	Asp	Glu	Ser	Pro 2875	Gln	Cys	Gly	Tyr	Arg 2880	Gln	Cys	Gly
Thr	Glu 2885	Glu	Phe	Ser	Cys	Ala 2890	Asp	Gly	Arg	Cys	Leu 2895	Leu	Asn	Thr
Gln	Trp 2900		Cys	Asp	Gly	Asp 2905	Phe	Asp	Cys	Pro	Asp 2910	His	Ser	Asp
Glu	Ala 2915	Pro	Leu	Asn	Pro	Lys 2920		Lys	Ser	Ala	Glu 2925	Gln	Ser	Cys
Asn	Ser 2930	Ser	Phe	Phe	Met	Cys 2935		Asn	Gly	Arg	Cys 2940	Ile	Pro	Ser
Gly	Gly 2945	Leu	Cys	Asp	Asn	Lys 2950	Asp	Asp	Cys	Gly	Asp 2955	Gly	Ser	Asp
Glu	Arg 2960		Cys	His	Ile	Asn 2965	Glu	Cys	Leu	Ser	Lys 2970	_	Val	Ser
Gly	Cys 2975		Gln	Asp	Cys	Gln 2980	_	Leu	Pro	Val	Ser 2985	_	Lys	Cys
Lys	Cys 2990	_	Pro	Gly	Phe	Gln 2995		Lys	Asp	Asp	Gly 3000	_	Thr	Cys
Val	Asp 3005		Asp	Glu	Cys	Ser 3010		Gly	Phe	Pro	Cys 3015		Gln	Gln

Cys Ile Asn Thr Tyr Gly Thr Tyr Lys Cys Leu Cys Thr Asp Gly 3020 3030

Tyr Glu Ile Gln Pro Asp Asn Pro Asn Gly Cys Lys Ser Leu Ser 3035 3040 3045

Asp Glu Glu Pro Phe Leu Ile Leu Ala Asp His His Glu Ile Arg 3050 3055 3060

Lys Ile Ser Thr Asp Gly Ser Asn Tyr Thr Leu Leu Lys Gln Gly 3065 3070 3075

Leu Asn Asn Val Ile Ala Ile Asp Phe Asp Tyr Arg Glu Glu Phe 3080 3085 3090

Ile Tyr Trp Ile Asp Ser Ser Arg Pro Asn Gly Ser Arg Ile Asn 3095 3100 3105

Arg Met Cys Leu Asn Gly Ser Asp Ile Lys Val Val His Asn Thr 3110 3115 3120

Ala Val Pro Asn Ala Leu Ala Val Asp Trp Ile Gly Lys Asn Leu 3125 3130 3135

Tyr Trp Ser Asp Thr Glu Lys Arg Ile Ile Glu Val Ser Lys Leu 3140 3145 3150

Asn Gly Leu Tyr Pro Thr Ile Leu Val Ser Lys Arg Leu Lys Phe 3155 3160 3165

Pro Arg Asp Leu Ser Leu Asp Pro Gln Ala Gly Tyr Leu Tyr Trp 3170 3175 3180

Ile Asp Cys Cys Glu Tyr Pro His Ile Gly Arg Val Gly Met Asp 3185 3190 3195

Gly Thr Asn Gln Ser Val Val Ile Glu Thr Lys Ile Ser Arg Pro 3200 3205 3210

Met Ala Leu Thr Ile Asp Tyr Val Asn Arg Arg Leu Tyr Trp Ala 3215 3220 3225

Asp Glu Asn His Ile Glu Phe Ser Asn Met Asp Gly Ser His Arg 3230 3240

His Lys Val Pro Asn Gln Asp Ile Pro Gly Val Ile Ala Leu Thr 3245 3250 3255

									, 0					
Leu	Phe 3260	Glu	Asp	Tyr	Ile	Tyr 3265	Trp	Thr	Asp	Gly	Lys 3270	Thr	Lys	Ser
Leu	Ser 3275	Arg	Ala	His	Lys	Thr 3280	Ser	Gly	Ala	Asp	Arg 3285	Leu	Ser	Leu
Ile	Tyr 3290	Ser	Trp	His	Ala	Ile 3295	Thr	Asp	Ile	Gln	Val 3300	Tyr	His	Ser
Tyr	Arg 3305	Gln	Pro	Asp	Val	Ser 3310	Lys	His	Leu	Cys	Met 3315	Ile	Asn	Asn
Gly	Gly 3320	_	Ser	His	Leu	Cys 3325	Leu	Leu	Ala	Pro	Gly 3330	Lys	Thr	His
Thr	Cys 3335		Cys	Pro	Thr	Asn 3340		Tyr	Leu	Ala	Ala 3345	Asp	Asn	Arg
Thr	Cys 3350		Ser	Asn	Cys	Thr 3355	Ala	Ser	Gln	Phe	Arg 3360	Cys	Lys	Thr
Asp	Lys 3365		Ile	Pro	Phe	Trp 3370		Lys	Cys	Asp	Thr 3375	Val	Asp	Asp
Cys	Gly 3380	_	Gly	Ser	Asp	Glu 3385		Asp	Asp	Cys	Pro 3390	Glu	Phe	Arg
Cys	Gln 3395		Gly	Arg	Phe	Gln 3400	Cys	Gly	Thr	Gly	Leu 3405	Cys	Ala	Leu
Pro	Ala 3410		Ile	Cys	Asp	Gly 3415		Asn	Asp	Cys	Gly 3420	Asp	Asn	Ser
Asp	Glu 3425		Asn	Cys	Asp	Thr 3430	His	Val	Cys	Leu	Ser 3435	Gly	Gln	Phe
Lys	Cys 3440		Lys	Asn	Gln	Lys 3445	_	Ile	Pro	Val	Asn 3450		Arg	Cys
Asn	Gly 3455		Asp	Asp	Cys	Gly 3460		Glu	Glu	Asp	Glu 3465		Asp	Cys
Pro	Glu 3470		Ser	Cys	Ser	Pro 3475	Asp	Tyr	Phe	Gln	Cys 3480	_	Thr	Thr

Lys His Cys Ile Ser Lys Leu Trp Val Cys Asp Glu Asp Pro Asp 3485

- Cys Ala Asp Ala Ser Asp Glu Ala Asn Cys Asp Lys Lys Thr Cys 3500 3505 3510
- Gly Pro His Glu Phe Gln Cys Lys Asn Asn Asn Cys Ile Pro Asp 3515 3520 3525
- His Trp Arg Cys Asp Ser Gln Asn Asp Cys Ser Asp Asn Ser Asp 3530 3535 3540
- Glu Glu Asn Cys Lys Pro Gln Thr Cys Thr Leu Lys Asp Phe Leu 3545 3550 3555
- Cys Ala Asn Gly Asp Cys Val Ser Ser Arg Phe Trp Cys Asp Gly 3560 3570
- Asp Phe Asp Cys Ala Asp Gly Ser Asp Glu Arg Asn Cys Glu Thr 3575 3580 3585
- Ser Cys Ser Lys Asp Gln Phe Arg Cys Ser Asn Gly Gln Cys Ile 3590 3595 3600
- Pro Ala Lys Trp Lys Cys Asp Gly His Glu Asp Cys Lys Tyr Gly 3605 3610 3615
- Glu Asp Glu Lys Ser Cys Glu Pro Ala Ser Pro Thr Cys Ser Ser 3620 3625 3630
- Arg Glu Tyr Ile Cys Ala Ser Asp Gly Cys Ile Ser Ala Ser Leu 3635 3640 3645
- Lys Cys Asn Gly Glu Tyr Asp Cys Ala Asp Gly Ser Asp Glu Met 3650 3660
- Asp Cys Val Thr Glu Cys Lys Glu Asp Gln Phe Arg Cys Lys Asn 3665 3670 3675
- Lys Ala His Cys Ile Pro Ile Arg Trp Leu Cys Asp Gly Ile His 3680 3685 3690
- Asp Cys Val Asp Gly Ser Asp Glu Glu Asn Cys Glu Arg Gly Gly 3695 3700 3705
- Asn Ile Cys Arg Ala Asp Glu Phe Leu Cys Asn Asn Ser Leu Cys 3710 3720
- Lys Leu His Phe Trp Val Cys Asp Gly Glu Asp Asp Cys Gly Asp 3725 3730 3735

- Asn Ser Asp Glu Ala Pro Asp Met Cys Val Lys Phe Leu Cys Pro 3740 3745 3750
- Ser Thr Arg Pro His Arg Cys Arg Asn Asn Arg Ile Cys Leu Gln 3755 3760 3765
- Ser Glu Gln Met Cys Asn Gly Ile Asp Glu Cys Gly Asp Asn Ser 3770 3775 3780
- Asp Glu Asp His Cys Gly Gly Lys Leu Thr Tyr Lys Ala Arg Pro 3785 3790 3795
- Cys Lys Lys Asp Glu Phe Ala Cys Ser Asn Lys Lys Cys Ile Pro 3800 3810
- Met Asp Leu Gln Cys Asp Arg Leu Asp Asp Cys Gly Asp Gly Ser 3815 3820 3825
- Asp Glu Gln Gly Cys Arg Ile Ala Pro Thr Glu Tyr Thr Cys Glu 3830 3840
- Asp Asn Val Asn Pro Cys Gly Asp Asp Ala Tyr Cys Asn Gln Ile 3845 3850 3855
- Lys Thr Ser Val Phe Cys Arg Cys Lys Pro Gly Phe Gln Arg Asn 3860 3865 3870
- Met Lys Asn Arg Gln Cys Glu Asp Leu Asn Glu Cys Leu Val Phe 3875 3880 3885
- Gly Thr Cys Ser His Gln Cys Ile Asn Val Glu Gly Ser Tyr Lys 3890 3895 3900
- Cys Val Cys Asp Gln Asn Phe Gln Glu Arg Asn Asn Thr Cys Ile 3905 3910 3915
- Ala Glu Gly Ser Glu Asp Gln Val Leu Tyr Ile Ala Asn Asp Thr 3920 3925 3930
- Asp Ile Leu Gly Phe Ile Tyr Pro Phe Asn Tyr Ser Gly Asp His 3935 3940 3945
- Gln Gln Ile Ser His Ile Glu His Asn Ser Arg Ile Thr Gly Met 3950 3960
- Asp Val Tyr Tyr Gln Arg Asp Met Ile Ile Trp Ser Thr Gln Phe 3965 3970 3975

- Asn Pro Gly Gly Ile Phe Tyr Lys Arg Ile His Gly Arg Glu Lys 3980 3985 3990
- Arg Gln Ala Asn Ser Gly Leu Ile Cys Pro Glu Phe Lys Arg Pro 3995 4000 4005
- Arg Asp Ile Ala Val Asp Trp Val Ala Gly Asn Ile Tyr Trp Thr 4010 4020
- Asp His Ser Arg Met His Trp Phe Ser Tyr Tyr Thr Thr His Trp 4025 4030 4035
- Thr Ser Leu Arg Tyr Ser Ile Asn Val Gly Gln Leu Asn Gly Pro $4040 \\ \hspace*{1.5cm} 4045 \\ \hspace*{1.5cm} 4050$
- Asn Cys Thr Arg Leu Leu Thr Asn Met Ala Gly Glu Pro Tyr Ala 4055 4060 4065
- Ile Ala Val Asn Pro Lys Arg Gly Met Met Tyr Trp Thr Val Val 4070 4075 4080
- Gly Asp His Ser His Ile Glu Glu Ala Ala Met Asp Gly Thr Leu 4085 4090 4095
- Arg Arg Ile Leu Val Gln Lys Asn Leu Gln Arg Pro Thr Gly Leu 4100 4105 4110
- Ala Val Asp Tyr Phe Ser Glu Arg Ile Tyr Trp Ala Asp Phe Glu 4115 4120 4125
- Leu Ser Ile Ile Gly Ser Val Leu Tyr Asp Gly Ser Asn Ser Val 4130 4135 4140
- Val Ser Val Ser Ser Lys Gln Gly Leu Leu His Pro His Arg Ile 4145 4150 4155
- Asp Ile Phe Glu Asp Tyr Ile Tyr Gly Ala Gly Pro Lys Asn Gly 4160 4170
- Val Phe Arg Val Gln Lys Phe Gly His Gly Ser Val Glu Tyr Leu 4175 4180 4185
- Ala Leu ·Asn Ile Asp Lys Thr Lys Gly Val Leu Ile Ser His Arg 4190 4195 4200
- Tyr Lys Gln Leu Asp Leu Pro Asn Pro Cys Leu Asp Leu Ala Cys 4205 4210 4215

Glu	Phe 4220	Leu	Cys	Leu	Leu	Asn 4225	Pro	Ser	Gly	Ala	Thr 4230	Cys	Val	Cys
Pro	Glu 4235	Gly	Lys	Tyr	Leu	Ile 4240	Asn	Gly	Thr	Cys	Asn 4245	Asp	Asp	Ser
Leu	Leu 4250		Asp	Ser		Lys 4255		Thr	Cys	Glu	Asn 4260	Gly	Gly	Arg
Cys	Ile 4265	Leu	Asn	Glu	Lys	Gly 4270	Asp	Leu	Arg	Cys	His 4275	Cys	Trp	Pro
Ser	Tyr 4280		Gly	Glu	Arg	Cys 4285		Val	Asn	His	Cys 4290	Ser	Asn	Tyr
Cys	Gln 4295		Gly	Gly	Thr	Cys 4300	Val	Pro	Ser	Val	Leu 4305	Gly	Arg	Pro
Thr	Cys 4310		Cys	Ala	Leu	Gly 4315		Thr	Gly	Pro	Asn 4320	Cys	Gly	Lys
Thr	Val 4325		Glu	Asp	Phe	Cys 4330		Asn	Gly	Gly	Thr 4335	Cys	Ile	Val
Thr	Ala 4340		Asn	Gln	Pro	Tyr 4345		His	Cys	Gln	Pro 4350	Glu	Tyr	Thr
Gly	Asp 4355		Cys	Glń	Tyr	Tyr 4360		Cys	His	His	Tyr 4365	Cys	Val	Asn
Ser	Glu 4370		Cys	Thr	Ile	Gly 4375		Asp	Gly	Ser	Leu 4380		Cys	Val
Cys	Pro 4385		Arg	Tyr	Glu	Gly 4390		Lys	Cys	Glu	Val 4395		Lys	Cys
Val	Arg 4400	_	His	Gly	Gly	His 4405		Ile	Ile	Asn	Lys 4410		Ser	Glu
Asp	Ile 4415		Cys	Asn	Cys	Thr 4420		Gly	Lys	Ile	Ala 4425		Ser	Cys
Gln	Leu 4430	_	Asp	Gly	Tyr	Cys 4435		Asn	Gly	Gly	Thr 4440		Gln	Leu
Asp	Pro 4445		Thr	Asn	Val	Pro 4450		Cys	Leu	Cys	Ser 4455		Asn	Trp

Ser Gly Thr Gln Cys Glu Arg Pro Ala Pro Lys Ser Ser Lys Ser 4465 Asp His Ile Ser Thr Arg Ser Ile Ala Ile Ile Val Pro Leu Val 4475 4480 . Leu Leu Val Thr Leu Ile Thr Thr Leu Val Ile Gly Leu Val Leu 4495 4490 Cys Lys Arg Lys Arg Arg Thr Lys Thr Ile Arg Arg Gln Pro Ile 4510 4505 Ile Asn Gly Gly Ile Asn Val Glu Ile Gly Asn Pro Ser Tyr Asn 4525 4520 Met Tyr Glu Val Asp His Asp His Asn Asp Gly Gly Leu Leu Asp 4545 4540 4535 Pro Gly Phe Met Ile Asp Pro Thr Lys Ala Arg Tyr Ile Gly Gly 4555 4550 Gly Pro Ser Ala Phe Lys Leu Pro His Thr Ala Pro Pro Ile Tyr 4575 4565 4570 Leu Asn Ser Asp Leu Lys Gly Pro Leu Thr Ala Gly Pro Thr Asn 4580 4585 Tyr Ser Asn Pro Val Tyr Ala Lys Leu Tyr Met Asp Gly Gln Asn 4595 4600 4605 Cys Arg Asn Ser Leu Gly Ser Val Asp Glu Arg Lys Glu Leu Leu 4610 Pro Lys Lys Ile Glu Ile Gly Ile Arg Glu Thr Val Ala 4630 <210> 34 <211> 2242 <212> DNA <213> Homo sapiens <220> <221> misc_feature <223> n = a or c or g or t <400> 34

gaatgeettt tagtgeettg etteetgaac tageteacag tageeeggeg geeeagggea 60
ateegaceac attteactet cacegetgta ggaateeaga tgeaggeeaa gtacageage 120

acgagggaca	tgctggatga	tgatggggac	accaccatga	gcctgcattc	tcaagcctct	180
gccacaactc	ggcatccaga	gccccggcgc	acagagcaca	gggctccctc	ttcaacgtgg	240
cgaccagtgg	ccctgaccct	gctgactttg	tgcttggtgc	tgctgatagg	gctggcagcc	300
ctggggcttt	tgttttttca	gtactaccag	ctctccaata	ctggtcaaga	caccatttct	360
caaatggaag	aaagattagg	aaatacgtcc	caagagttgc	aatctcttca	agtccagaat	420
ataaagcttg	caggaagtct	gcagcatgtg	gctgaaaaac	tctgtcgtga	gctgtataac	480
aaagctggag	cacacaggtg	cagcccttgt	acagaacaat	ggaaatggca	tggagacaat	540
tgctaccagt	tctataaaga	cagcaaaagt	tgggaggact	gtaaatattt	ctgccttagt	600
gaaaactcta	ccatgctgaa	gataaacaaa	caagaagacc	tggaatttgc	cgcgtctcag	660
agctactctg	agtttttcta	ctcttattgg	acagggcttt	tgcgccctga	cagtggcaag	720
gcctggctgt	ggatggatgg	aacccctttc	acttctgaac	tgttccatat	tataatagat	780
gtcaccagcc	caagaagcag	agactgtgtg	gccatcctta	atgggatgat	cttctcaaag	840
gactgcaaag	aattgaagcg	ttgtgtctgt	gagagaaggg	caggaatggt	gaagccagag	900
agcctccatg	tcccccctga	aacattaggc	gaaggtgact	gattcgccct	ctgcaactac	960
aaatagcaga	gtgagccagg	cggtgccaaa	gcaagggcta	gttgagacat	tgggaaatgg	1020
aacataatca	ggaaagacta	tctctctgac	tagtacaaaa	tgggttctcg	tgtttcctgt	1080
tcaggatcac	cagcatttct	gagcttgggt	ttatgcacgt	atttaacagt	cacaagaagt	1140
cttatttaca	tgccaccaac	caacctcaga	aacccataat	gtcatctgcc	ttcttggctt	1200
agagataact	tttagctctc	tttcttctca	atgtctaata	tcacctccct	gttttcatgt	1260
cttccttaca	cttggtggaa	taagaaactt	tttgaagtag	aggaaataca	ttgaggtaac	1320
atccttttct	ctgacagtca	agtagtccat	cagaaattgg	cagtcacttc	ccagattgta	1380
ccagcaaata	cacaaggaat	tctttttgtt	tgtttcagtt	catactagtc	ccttcccaat	1440
ccatcagtaa	agaccccatc	tgccttgtcc	atgccgtttc	ccaacaggga	tgtcacttga	1500
tatgagaatc	tcaaatctca	atgccttata	agcattcctt	cctgtgtcca	ttaagactct	1560
gataattgtc	tcccctccat	aggaatttct	cccaggaaag	aaatatatcc	ccatctccgt	1620
ttcatatcag	aactaccgtc	cccgatattc	ccttcagaga	gattaaagac	cagaaaaaag	1680
tgagcctctt	catctgcacc	tgtaatagtt	tcagttccta	ttttcttcca	ttgacccata	1740
tttatacctt	tcaggtactg	aagatttaat	aataataaat	gtaaatactg	tgaagtgtgt	1800
gtgattttac	aatggactta	tggttggtgg	gaaaattcag	catggaaatg	cttttcaaaa	1860
tatgatagcg	gtcattattt	tgattgtgcc	ttactgaaag	tttttgggga	atttacaaga	1920
gtactgatta	catgattatc	tggagaaaat	aagatgtctt	tgaaatacat	gttggcttca	1980
agaaaacagt	tttaacgttt	tcctaaaatg	aaatcttttg	aggtgagctt	atggcatcaa	2040

cacatggttg	atgaggaagc	tgagttgcat	tagtgcacat	gatttccagt	caggtcatgg	2100
gaaatgaaca	gagacagtga	catctttgta	gctgctcctt	tgtgaggcac	ttctttcttg	2160
agatgactcc	atgcacaaat	ataacaggga	tcattgggaa	tgacaccatc	acagccacca	2220
agnttattgg	gttactgata	at				2242

<210> 35

<211> 280

<212> PRT

<213> Homo sapiens

<400> 35

Met Gln Ala Lys Tyr Ser Ser Thr Arg Asp Met Leu Asp Asp Gly 1 10 15

Asp Thr Thr Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr Arg His 20 25 30

Pro Glu Pro Arg Arg Thr Glu His Arg Ala Pro Ser Ser Thr Trp Arg 35 40 45

Pro Val Ala Leu Thr Leu Leu Thr Leu Cys Leu Val Leu Leu Ile Gly 50 60

Leu Ala Ala Leu Gly Leu Leu Phe Phe Gln Tyr Tyr Gln Leu Ser Asn 65 70 75 80

Thr Gly Gln Asp Thr Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr 85 90 95

Ser Gln Glu Leu Gln Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly 100 105 110

Ser Leu Gln His Val Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys 115 120 125

Ala Gly Ala His Arg Cys Ser Pro Cys Thr Glu Gln Trp Lys Trp His 130 135 140

Gly Asp Asn Cys Tyr Gln Phe Tyr Lys Asp Ser Lys Ser Trp Glu Asp 145 150 155 160

Cys Lys Tyr Phe Cys Leu Ser Glu Asn Ser Thr Met Leu Lys Ile Asn 165 170 175

Lys Gln Glu Asp Leu Glu Phe Ala Ala Ser Gln Ser Tyr Ser Glu Phe 180 185 190

Phe Tyr Ser Tyr Trp Thr Gly Leu Arg Pro Asp Ser Gly Lys Ala 195 200 205

Trp Leu Trp Met Asp Gly Thr Pro Phe Thr Ser Glu Leu Phe His Ile 210 215 220

Ile Ile Asp Val Thr Ser Pro Arg Ser Arg Asp Cys Val Ala Ile Leu 225 230 235 240

As Gly Met Ile Phe Ser Lys Asp Cys Lys Glu Leu Lys Arg Cys Val $245 \hspace{1.5cm} 250 \hspace{1.5cm} 255$

Cys Glu Arg Arg Ala Gly Met Val Lys Pro Glu Ser Leu His Val Pro 260 265 270

Pro Glu Thr Leu Gly Glu Gly Asp 275 280

<210> 36

<211> 2323

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

 $\langle 223 \rangle$ n = a or c or g or t

<400> 36 gaatgccttt tagtgccttg cttcctgaac tagctcacag tagcccggcg gcccagggca 60 atccgaccac atttcactct caccgctgta ggaatccaga tgcaggccaa gtacagcagc 120 acgagggaca tgctggatga tgatggggac accaccatga gcctgcattc tcaagcctct 180 gccacaactc ggcatccaga gccccggcgc acagagcaca gggctccctc ttcaacgtgg 240 300 cgaccagtgg ccctgacctt gctgactttg tgcttggtgc tgctgatagg gctggcagcc ctqqqqcttt tqttttttca qtactaccag ctctccaata ctggtcaaga caccatttct 360 420 caaatggaag aaagattagg aaatacgtcc caagagttgc aatctcttca agtccagaat 480 ataaaqcttq caqqaaqtct gcagcatgtg gctgaaaaac tctgtcgtga gctgtataac 540 aaaqctqqaq qctatacaaq aaacatqqtq ccaqcatctq cttcttctga gagcctcagg cagcttccac acatggggga aagtgcagca gcacacaggt gcagcccttg tacagaacaa 600 660 tqqaaatqqc atqqaqacaa ttqctaccag ttctataaag acagcaaaag ttgggaggac 720 tgtaaatatt tctgccttag tgaaaactct accatgctga agataaacaa acaagaagac 780 ctggaatttg ccgcgtctca gagctactct gagtttttct actcttattg gacagggctt ttgcgccctg acagtggcaa ggcctggctg tggatggatg gaaccccttt cacttctgaa 840 900 ctgttccata ttataataga tgtcaccagc ccaagaagca gagactgtgt ggccatcctt aatgggatga tottotcaaa ggactgcaaa gaattgaago gttgtgtctg tgagagaagg 960 gcaggaatgg tgaagccaga gagcctccat gtcccccctg aaacattagg cgaaggtgac 1020 1080 tgattcgccc tctgcaacta caaatagcag agtgagccag gcggtgccaa agcaagggct agttgagaca ttgggaaatg gaacataatc aggaaagact atctctctga ctagtacaaa 1140 atgggttctc gtgtttcctg ttcaggatca ccagcatttc tgagcttggg tttatgcacg 1200 tatttaacaq tcacaaqaaq tcttatttac atqccaccaa ccaacctcaq aaacccataa 1260 tgtcatctgc cttcttggct tagagataac ttttagctct ctttcttctc aatgtctaat 1320 atcacctccc tgttttcatg tcttccttac acttggtgga ataagaaact ttttgaagta 1380

gaggaaatac	attgaggtaa	catccttttc	tctgacagtc	aagtagtcca	tcagaaattg	1440
gcagtcactt	cccagattgt	accagcaaat	acacaaggaa	ttctttttgt	ttgtttcagt	1500
tcatactagt	cccttcccaa	tccatcagta	aagaccccat	ctgccttgtc	catgccgttt	1560
cccaacaggg	atgtcacttg	atatgagaat	ctcaaatctc	aatgccttat	aagcattcct	1620
tcctgtgtcc	attaagactc	tgataattgt	ctccctcca	taggaatttc	tcccaggaaa	1680
gaaatatatc	cccatctccg	tttcatatca	gaactaccgt	ccccgatatt	cccttcagag	1740
agattaaaga	ccagaaaaaa	gtgagcctct	tcatctgcac	ctgtaatagt	ttcagttcct	1800
attttcttcc	attgacccat	atttatacct	ttcaggtact	gaagatttaa	taataataaa	1860
tgtaaatact	gtgaagtgtg	tgtgatttta	caatggactt	atggttggtg	ggaaaattca	1920
gcatggaaat	gcttttcaaa	atatgatagc	ggtcattatt	ttgattgtgc	cttactgaaa	1980
gtttttgggg	aatttacaag	agtactgatt	acatgattat	ctggagaaaa	taagatgtct	2040
ttgaaataca	tgttggcttc	aagaaaacag	ttttaacgtt	ttcctaaaat	gaaatctttt	2100
gaggtgagct	tatggcatca	acacatggtt	gatgaggaag	ctgagttgca	ttagtgcaca	2160
tgatttccag	tcaggtcatg	ggaaatgaac	agagacagtg	acatctttgt	agctgctcct	2220
ttgtgaggca	cttctttctt	gagatgactc	catgcacaaa	tataacaggg	atcattggga	2280
atgacaccat	cacagecace	aagnttattg	ggttactgat	aat		2323

<210> 37 <211> 307 <212> PRT <213> Homo sapiens

<400> 37

Asp Thr Thr Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr Arg His 20 25 30

Pro Glu Pro Arg Arg Thr Glu His Arg Ala Pro Ser Ser Thr Trp Arg 35 40 45

Pro Val Ala Leu Thr Leu Leu Thr Leu Cys Leu Val Leu Leu Ile Gly 50 55 60

Leu Ala Ala Leu Gly Leu Leu Phe Phe Gln Tyr Tyr Gln Leu Ser Asn 65 70 75 80

Thr Gly Gln Asp Thr Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr 85 90 95

Ser Gln Glu Leu Gln Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly 100 105 110

Ser Leu Gln His Val Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys 115 120 125

Ala Gly Gly Tyr Thr Arg Asn Met Val Pro Ala Ser Ala Ser Ser Glu 130 135 140	
Ser Leu Arg Gln Leu Pro His Met Gly Glu Ser Ala Ala Ala His Arg 145 150 155 160	
Cys Ser Pro Cys Thr Glu Gln Trp Lys Trp His Gly Asp Asn Cys Tyr 165 170 175	
Gln Phe Tyr Lys Asp Ser Lys Ser Trp Glu Asp Cys Lys Tyr Phe Cys 180 185 190	
Leu Ser Glu Asn Ser Thr Met Leu Lys Ile Asn Lys Gln Glu Asp Leu 195 200 205	
Glu Phe Ala Ala Ser Gln Ser Tyr Ser Glu Phe Phe Tyr Ser Tyr Trp 210 215 220	
Thr Gly Leu Leu Arg Pro Asp Ser Gly Lys Ala Trp Leu Trp Met Asp 225 230 235 240	
Gly Thr Pro Phe Thr Ser Glu Leu Phe His Ile Ile Ile Asp Val Thr 245 250 255	
Ser Pro Arg Ser Arg Asp Cys Val Ala Ile Leu Asn Gly Met Ile Phe 260 265 270	
Ser Lys Asp Cys Lys Glu Leu Lys Arg Cys Val Cys Glu Arg Arg Ala 275 280 285	
Gly Met Val Lys Pro Glu Ser Leu His Val Pro Pro Glu Thr Leu Gly 290 295 300	
Glu Gly Asp 305	
<210> 38 <211> 2714 <212> DNA	
<213> Homo sapiens	
<400> 38 gaatcgagcc cgacgtcgca tgctcccggc cgccatggcc gcgggattcc cgggtcgacg	60
atttcgtcgg gaggaatgga aggagaaggc ggaatgtggg agggctcagg gggatgtggg	120
agggacgaac ggagaagggg gagagagggg ggtccagtct cccctggccg agcatttttt	180
ttttggaagt cctaggactg atctccagga ccagcactct tctcccagcc cttagggtcc	240
tgctcggcca aggccttccc tgccatgcga cctgtcagtg tctggcagtg gagccctgg	300
gggetgetge tgtgeetget gtgeagtteg tgettggggt etcegteece tteeaeggge	360
cctgagaaga aggccgggag ccaggggctt cggttccggc tggctggctt ccccaggaag	420
ccctacgagg gccgcgtgga gatacagcga gctggtgaat ggggcaccat ctgcgatgat	480
gacttcacge tgcaggetge ceacateete tgcegggage tgggetteae agaggecaea	540
ggctggaccc acagtgccaa atatggccct ggaacaggcc gcatctggct ggacaacttg	600
agetgeagtg ggacegagea gagtgtgaet gaatgtgeet eeeggggetg ggggaacagt	660

gactgtacgc	acgatgagga	tgctggggtc	atctgcaaag	accagcgcct	ccctggcttc	720
teggaeteca	atgtcattga	ggtagagcat	cacctgcaag	tggaggaggt	gcgaattcga	780
cccgccgttg	ggtggggcag	acgacccctg	cccgtgacgg	aggggctggt	ggaagtcagg	840
cttcctgacg	gctggtcgca	agtgtgcgac	aaaggctgga	gcgcccacaa	cagccacgtg	900
gtctgcggga	tgctgggctt	ccccagcgaa	aagagggtca	acgcggcctt	ctacagaaag	960
ttgaggaagc	gagcggccaa	ggtctcagcc	cgacacccca	agccccttgg	aaggctgcta	1020
gcccaacggc	agcaacactc	ctttggtctg	catggggtgg	cgtgcgtggg	cacggaggcc	1080
cacctctccc	tctgttccct	ggagttctat	cgtgccaatg	acaccgccag	gtgccctggg	1140
gggggccctg	cagtggtgag	ctgtgtgcca	ggccctgtct	acgcggcatc	cagtggccag	1200
aagaagcaac	aacagtcgaa	gcctcagggg	gaggcccgtg	tccgtctaaa	gggcggcgcc	1260
caccctggag	agggccgggt	agaagtcctg	aaggccagca	catggggcac	agtctgtgac	1320
cgcaagtggg	acctgcatgc	agccagcgtg	gtgtgtcggg	agctgggctt	cgggagtgct	1380
cgagaagctc	tgagtggcgc	tcgcatgggg	cagggcatgg	gtgctatcca	cctgagtgaa	1440
gttcgctgct	ctggacagga	gctctccctc	tggaagtgcc	cccacaagaa	catcacagct	1500
gaggattgtt	cacatagcca	ggatgccggg	gtccggtgca	acctacctta	cactggggca	1560
gagaccagga	tccgactcag	tgggggccgc	agccaacatg	aggggcgagt	cgaggtgcaa	1620
atagggggac	ctgggcccct	tegetgggge	ctcatctgtg	gggatgactg	ggggaccctg	1680
gaggccatgg	tggcctgtag	gcaactgggt	ctgggctacg	ccaaccacgg	cctgcaggag	1740
acctggtact	gggactctgg	gaatataaca	gaggtggtga	tgagtggagt	gcgctgcaca	1800
gggactgagc	tgtccctgga	tcagtgtgcc	catcatggca	cccacatcac	ctgcaagagg	1860
acagggaccc	gcttcactgc	tggagtcatc	tgttctgaga	ctgcatcaga	tctgttgctg	1920
cactcagcac	tggtgcagga	gaccgcctac	atcgaagacc	ggcccctgca	tatgttgtac	1980
tgtgctgcgg	aagagaactg	cctggccagc	tcagcccgct	cagccaactg	gccctatggt	2040
caccggcgtc	tgctccgatt	ctcctcccag	atccacaacc	tgggacgagc	tgacttcagg	2100
cccaaggctg	ggcgccactc	ctgggtgtgg	cacgagtgcc	atgggcatta	ccacagcatg	2160
gacatcttca	ctcactatga	tatcctcacc	ccaaatggca	ccaaggtggc	tgagggccac	2220
aaagctagtt	tctgtctcga	agacactgag	tgtcaggagg	atgtctccaa	gcggtatgag	2280
tgtgccaact	ttggagagca	aggcatcact	gtgggttgct	gggatctcta	ccggcatgac	2340
attgactgtc	agtggattga	catcacggat	gtgaagccag	gaaactacat	tctccaggtt	2400
gtcatcaacc	caaactttga	agtagcagag	agtgacttta	ccaacaatgc	aatgaaatgt	2460
aactgcaaat	atgatggaca	tagaatctgg	gtgcacaact	gccacattgg	tgatgccttc	2520
agtgaagagg	cccacaggag	gtttgaacgc	tcccctggcc	agaccagcac	ctagattatg	2580

taagtgccac	tgccctttgc	aaaccgcccc	tggcgcctaa	tggcaggggt	ctgaggctgc	2640
cattacctca	ggagcttatc	aagaaaccca	tgtcagcaac	catgtattgc	ggccgctcta	2700
gaggaatcgc	cagc					2714

<210> 39 <211> 769 <212> PRT <213> Homo sapiens

<400> 39

Met Arg Pro Val Ser Val Trp Gln Trp Ser Pro Trp Gly Leu Leu 1 5 10 15

Cys Leu Leu Cys Ser Ser Cys Leu Gly Ser Pro Ser Pro Ser Thr Gly
20 25 30

Pro Glu Lys Lys Ala Gly Ser Gln Gly Leu Arg Phe Arg Leu Ala Gly 35 40 45

Phe Pro Arg Lys Pro Tyr Glu Gly Arg Val Glu Ile Gln Arg Ala Gly 50 55 60

Glu Trp Gly Thr Ile Cys Asp Asp Asp Phe Thr Leu Gln Ala Ala His 65 70 75 80

Ile Leu Cys Arg Glu Leu Gly Phe Thr Glu Ala Thr Gly Trp Thr His 85 90 95

Ser Ala Lys Tyr Gly Pro Gly Thr Gly Arg Ile Trp Leu Asp Asn Leu 100 105 110

Ser Cys Ser Gly Thr Glu Gln Ser Val Thr Glu Cys Ala Ser Arg Gly 115 120 125

Trp Gly Asn Ser Asp Cys Thr His Asp Glu Asp Ala Gly Val Ile Cys 130 140

Lys Asp Gln Arg Leu Pro Gly Phe Ser Asp Ser Asn Val Ile Glu Val 145 150 155 160

Glu His His Leu Gln Val Glu Glu Val Arg Ile Arg Pro Ala Val Gly 165 170 175

Trp Gly Arg Arg Pro Leu Pro Val Thr Glu Gly Leu Val Glu Val Arg
180 185 190

Leu Pro Asp Gly Trp Ser Gln Val Cys Asp Lys Gly Trp Ser Ala His 195 200 205

Asn Ser His Val Val Cys Gly Met Leu Gly Phe Pro Ser Glu Lys Arg 210 215 220

Val Asn Ala Ala Phe Tyr Arg Lys Leu Arg Lys Arg Ala Ala Lys Val 225 230 235 240

Ser Ala Arg His Pro Lys Pro Leu Gly Arg Leu Leu Ala Gln Arg Gln 245 250 255

Gln His Ser Phe Gly Leu His Gly Val Ala Cys Val Gly Thr Glu Ala

270 260 265 His Leu Ser Leu Cys Ser Leu Glu Phe Tyr Arg Ala Asn Asp Thr Ala Arg Cys Pro Gly Gly Pro Ala Val Val Ser Cys Val Pro Gly Pro Val Tyr Ala Ala Ser Ser Gly Gln Lys Lys Gln Gln Gln Ser Lys Pro Gln Gly Glu Ala Arg Val Arg Leu Lys Gly Gly Ala His Pro Gly Glu Gly Arg Val Glu Val Leu Lys Ala Ser Thr Trp Gly Thr Val Cys Asp 345 Arg Lys Trp Asp Leu His Ala Ala Ser Val Val Cys Arg Glu Leu Gly 360 Phe Gly Ser Ala Arg Glu Ala Leu Ser Gly Ala Arg Met Gly Gln Gly 375 Met Gly Ala Ile His Leu Ser Glu Val Arg Cys Ser Gly Gln Glu Leu Ser Leu Trp Lys Cys Pro His Lys Asn Ile Thr Ala Glu Asp Cys Ser His Ser Gln Asp Ala Gly Val Arg Cys Asn Leu Pro Tyr Thr Gly Ala 425 Glu Thr Arg Ile Arg Leu Ser Gly Gly Arg Ser Gln His Glu Gly Arg Val Glu Val Gln Ile Gly Gly Pro Gly Pro Leu Arg Trp Gly Leu Ile Cys Gly Asp Asp Trp Gly Thr Leu Glu Ala Met Val Ala Cys Arg Gln Leu Gly Leu Gly Tyr Ala Asn His Gly Leu Gln Glu Thr Trp Tyr Trp Asp Ser Gly Asn Ile Thr Glu Val Val Met Ser Gly Val Arg Cys Thr 505 Gly Thr Glu Leu Ser Leu Asp Gln Cys Ala His His Gly Thr His Ile 520 Thr Cys Lys Arg Thr Gly Thr Arg Phe Thr Ala Gly Val Ile Cys Ser Glu Thr Ala Ser Asp Leu Leu His Ser Ala Leu Val Gln Glu Thr 550 Ala Tyr Ile Glu Asp Arg Pro Leu His Met Leu Tyr Cys Ala Ala Glu Glu Asn Cys Leu Ala Ser Ser Ala Arg Ser Ala Asn Trp Pro Tyr Gly 585

His Arg Arg Leu Leu Arg Phe Ser Ser Gln Ile His Asn Leu Gly Arg

605

600

ggggaagaca ccaaggccca gttgctgggg ggcgtggacg aggcttgggc tttqctqcaq

660

595

ggactgcaga	gccgcgtggt	gcaccacacc	ggccgcttca	aagagctctt	ccacccatac	720
gccgagagcc	tggtgagcgg	catcgggcgc	cacgtgcagg	agctgcaccg	cagtgtggct	780
ccgcacgccc	ccgccagccc	cgcgcgcctc	agtcgctgcg	tgcaggtgct	ctcccggaag	840
ctcacgctca	aggccaaggc	cctgcacgca	cgcatccagc	agaacctgga	ccagctgcgc	900
gaagagctca	gcagagcctt	tgcaggcact	gggactgagg	aaggggccgg	cccggacccc	960
cagatgctct	ccgaggaggt	gcgccagcga	cttcaggctt	tccgccagga	cacctacctg	1020
cagatagctg	ccttcactcg	cgccatcgac	caggagactg	aggaggtcca	gcagcagctg	1080
gcgccacctc	caccaggcca	cagtgccttc	gccccagagt	ttcaacaaac	agacagtggc	1140
aaggttctga	gcaagctgca	ggcccgtctg	gatgacctgt	gggaagacat	cactcacagc	1200
cttcatgacc	agggccacag	ccatctgggg	gacccctgag	gatctacctg	cccaggccca	1260
ttcccagctc	cttgtctggg	gagccttggc	tctgagcctc	tagcatggtt	cagtccttga	1320
aagtggcctg	ttgggtggag	ggtggaaggt	cctgtgcagg	acagggaggc	caccaaaggg	1380
gctgctgtct	cctgcacatc	cagcctcctg	cgactcccca	atctggatgc	attacattca	1440
ccaggctttg	caaacccagc	ctcccagtgc	tcatttggga	atgctcatga	gttactccat	1500
tcaagggtga	gggagtaggg	agggagaggc	accatgcatg	tgggtgatta	tctgcaagcc	1560
tgtttgccgt	gatgctggaa	gcctgtgcca	ctacatcctg	gagtctgaca	ctgagcccct	1620
gcgagtgacc	gtgagcacac	agttccgtag	cggggcccat	acgagactcg	acgcgcgcgc	1680
accacgaggt	cccgagggag	gacactcgac	ggacacgagt	gacgggaaat	gtgcatctac	1740
actagcgcgc	gacagctaga	gcgatgacgg	cgaggacgtc	tcgcagccta	ccagcaacgc	1800
gaagacgtgc	ctcccggcgt	cgtatggatt	aacaagctcc	aagtagggtg	tacaacgccg	1860
cagcatgaac	tcccagg					1877

Met Asn Lys Lys Pro Leu His Ser Lys Ser Ser Arg Ile His Gln

Gln Ile Ile Val Gln Leu Asp Ser Leu Pro Pro Pro Val Phe Ser Glu 25

Gln Val Met Ala Ser Met Ala Ala Val Leu Thr Trp Ala Leu Ala Leu

Leu Ser Ala Phe Ser Ala Thr Gln Ala Arg Lys Gly Phe Trp Asp Tyr

Phe Ser Gln Thr Ser Gly Asp Lys Gly Arg Val Glu Gln Ile His Gln

<210> 41 <211> 400 <212> PRT

<213> Homo sapiens

<400> 41

70 75 65 80 Gln Lys Met Ala Arg Glu Pro Ala Thr Leu Lys Asp Ser Leu Glu Gln Asp Leu Asn Asn Met Asn Lys Phe Leu Glu Lys Leu Arg Pro Leu Ser 105 Gly Ser Glu Ala Pro Arg Leu Pro Gln Asp Pro Val Gly Met Arg Arg 120 Gln Leu Gln Glu Leu Glu Glu Val Lys Ala Arg Leu Gln Pro Tyr Met Ala Glu Ala His Glu Leu Val Gly Trp Asn Leu Glu Gly Leu Arg 150 Gln Gln Leu Lys Pro Tyr Thr Met Asp Leu Met Glu Gln Val Ala Leu Arg Val Gln Glu Leu Gln Glu Gln Leu Arg Val Val Gly Glu Asp Thr 180 Lys Ala Gln Leu Leu Gly Gly Val Asp Glu Ala Trp Ala Leu Leu Gln Gly Leu Gln Ser Arg Val Val His His Thr Gly Arg Phe Lys Glu Leu 215 Phe His Pro Tyr Ala Glu Ser Leu Val Ser Gly Ile Gly Arg His Val 230 Gln Glu Leu His Arg Ser Val Ala Pro His Ala Pro Ala Ser Pro Ala Arg Leu Ser Arg Cys Val Gln Val Leu Ser Arg Lys Leu Thr Leu Lys Ala Lys Ala Leu His Ala Arg Ile Gln Gln Asn Leu Asp Gln Leu Arg 280 Glu Glu Leu Ser Arg Ala Phe Ala Gly Thr Gly Thr Glu Glu Gly Ala Gly Pro Asp Pro Gln Met Leu Ser Glu Glu Val Arg Gln Arg Leu Gln Ala Phe Arg Gln Asp Thr Tyr Leu Gln Ile Ala Ala Phe Thr Arg Ala 330 Ile Asp Gln Glu Thr Glu Glu Val Gln Gln Leu Ala Pro Pro Pro Gly His Ser Ala Phe Ala Pro Glu Phe Gln Gln Thr Asp Ser Gly 360 Lys Val Leu Ser Lys Leu Gln Ala Arg Leu Asp Asp Leu Trp Glu Asp Ile Thr His Ser Leu His Asp Gln Gly His Ser His Leu Gly Asp Pro 395 <210> 42

<211> 2128 <212> DNA

<213> Homo sapiens

<400> 42 gcaccggtcc ggaattcccg ggtcgacgat ttcgtctcaa cattcagcag aggccccaga 60 tcagcgtctg agccaggcca acaatgacca aggaggatgg gatcctgggt gcagctcatc 120 acaagcgtcg gggtgcagca aaaccatcca ggctggacag tggctggaca gttccaagaa 180 , aagaaacgct tcactgaaga agtcattgaa tacttccaga agaaagttag cccagtgcat 240 ctgaaaatcc tgctgactag cgatgaagcc tggaagagat ttgtgcgtgt ggctgaattg 300 360 cccagggaag aggcagatgc tctctatgaa gctctgaaga atcttacacc atatgtgact 420 attgaggaca aagacatgca gcaaaaagaa cagcagttta gggagtggtt tttgaaagag tttcctcaaa tcagatggaa gattcaggag tccatagaaa ggcttcgtgt cattgcaaat 480 gagattgaaa aggtccacag aggctgcgtc atcgccaatg tggtgtctgg ctccactggc 540 600 atcctgtctg tcattggcgt tatgttggca ccatttacag cagggctgag cctgagcatt actgcagctg gggtagggct gggaatagca tctgccacgg ctgggatcgc ctccagcatc 660 720 gtggagaaca catacacaag gtcagcagaa ctcacagcca gcaggctgac tgcaaccagc actgaccaat tggaggcatt aagggacatt ctgcatgaca tcacacccaa tgtgctttcc 780 840 tttgcacttg attttgacga agccacaaaa atgattgcga atgatgtcca tacactcagg agatetaaag ceaetgttgg aegeeetttg attgettgge gatatgtaee tataaatgtt 900 960 gttgagacac tgagaacacg tggggccccc acccggatag tgagaaaagt agcccggaac ctgggcaagg ccacttcagg tgtccttgtt gtgctggatg tagtcaacct tgtgcaagac 1020 tcactggact tgcacaaggg ggcaaaatcc gagtctgctg agtcgctgag gcagtgggct 1080 caggagetgg aggagaatet caatgagete acceatatee ateagagtet aaaageagge 1140 taggcccaat tgttgcggga agtcagggac cccaaacgga gggactggct gaagccatgg 1200 cagaagaacg tggattgtga agatttcatg gacatttatt agttccccaa attaatactt 1260 ttataatttc ctatgcctgt ctttaccgca atctctaaac acaaattgtg aagatttcat 1320 1380 atctcctaat cctgtcagct gaggaggatg tatgtcacct caggaccatg tgataattgc 1440 gttaactgca caaattgtag agcatgtgtg tttgaacaat atgaaatctg ggcaccttga 1500 aaaaagaaca ggataacagc aattgttcag ggaataagag agataacctt aaactctgac 1560 caacagtgag ccgggtggaa cagagtcata tttctcttct ttcaaaagca aatgggagaa 1620 atatcgctga attctttttc tcagcaagga acatccctga gaaagagaat gcaccctga 1680 gggtgggtct ataaatggcc tccttgggtg tggccatctt ctatggtcga gactgtaggg 1740

atgaaataaa	ccccagtctc	ccatagtgct	cccaggctta	ttaggaagag	gaaattcccg	1800
cctaataaat	tttggtcaga	ccggttgctc	tcaaaaccct	gtctcctgat	aagatgttat	1860
caatgacaat	ggtgcctgaa	acctcattag	caattttaat	ttctccccgg	tcctgtggtc	1920
ctgtgatctc	accctgcctc	cacttgcctt	gtgatattct	attaccttgt	gaagtaggtg	1980
atctttgtga	cccacaccct	attcatacac	tccctcccct	tttgaaagtc	cctaataaaa	2040
acttgctggt	tttgcagctt	gtgaggcatc	acggaaccta	ctgatgtgtg	atgtctcccc	2100
tggacaccta	gctttaaaat	ttcaaaaa				2128

<210> 43 <211> 348 <212> PRT <213> Homo sapiens

<400> 43

Met Gly Ser Trp Val Gln Leu Ile Thr Ser Val Gly Val Gln Gln Asn 1 5 10 15

His Pro Gly Trp Thr Val Ala Gly Gln Phe Gln Glu Lys Lys Arg Phe 20 25 30

Thr Glu Glu Val Ile Glu Tyr Phe Gln Lys Lys Val Ser Pro Val Hıs 35 40 45

Leu Lys Ile Leu Leu Thr Ser Asp Glu Ala Trp Lys Arg Phe Val Arg 50 55 60

Val Ala Glu Leu Pro Arg Glu Glu Ala Asp Ala Leu Tyr Glu Ala Leu 65 70 75 80

Lys Asn Leu Thr Pro Tyr Val Thr Ile Glu Asp Lys Asp Met Gln Gln 85 90 95

Lys Glu Gln Gln Phe Arg Glu Trp Phe Leu Lys Glu Phe Pro Gln Ile 100 105 110

Arg Trp Lys Ile Gln Glu Ser Ile Glu Arg Leu Arg Val Ile Ala Asn 115 120 125

Glu Ile Glu Lys Val His Arg Gly Cys Val Ile Ala Asn Val Val Ser 130 135 140

Gly Ser Thr Gly Ile Leu Ser Val Ile Gly Val Met Leu Ala Pro Phe 145 150 155 160

Thr Ala Gly Leu Ser Leu Ser Ile Thr Ala Ala Gly Val Gly Leu Gly 165 170 175

Ile Ala Ser Ala Thr Ala Gly Ile Ala Ser Ser Ile Val Glu Asn Thr

Tyr Thr Arg Ser Ala Glu Leu Thr Ala Ser Arg Leu Thr Ala Thr Ser 195 200 205

Thr Asp Gln Leu Glu Ala Leu Arg Asp Ile Leu His Asp Ile Thr Pro 210 215 220

Asn Val Leu Ser Phe Ala Leu Asp Phe Asp Glu Ala Thr Lys Met Ile 225 230 235 240	
Ala Asn Asp Val His Thr Leu Arg Arg Ser Lys Ala Thr Val Gly Arg 245 250 255	
Pro Leu Ile Ala Trp Arg Tyr Val Pro Ile Asn Val Val Glu Thr Leu 260 265 270	
Arg Thr Arg Gly Ala Pro Thr Arg Ile Val Arg Lys Val Ala Arg Asn 275 280 285	
Leu Gly Lys Ala Thr Ser Gly Val Leu Val Val Leu Asp Val Val Asn 290 295 300	
Leu Val Gln Asp Ser Leu Asp Leu His Lys Gly Ala Lys Ser Glu Ser 305 310 315 320	
Ala Glu Ser Leu Arg Gln Trp Ala Gln Glu Leu Glu Glu Asn Leu Asn 325 330 335	
Glu Leu Thr His Ile His Gln Ser Leu Lys Ala Gly 340 345	
<210> 44 <211> 988 <212> DNA <213> Homo sapiens	
<220> <221> misc_feature <223> n = a or c or g or t	
<220> <221> CDS <222> (129)(971)	
<400> 44 agagctgccg gngnnnnaat ggatagaata ctcttgacca nngacgcacg agcctgaact	60
ageteacagt ageceggegg eccagggeaa teegaceaca ttteactete accgetgtag	120
gaatccag atg cag gcc aag tac agc agc acg agg gac atg ctg gat gat	
Met Gln Ala Lys Tyr Ser Ser Thr Arg Asp Met Leu Asp Asp 1 5 10	170
	170 218
gat ggg gac acc acc atg agc ctg cat tct caa gcc tct gcc aca act Asp Gly Asp Thr Thr Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr	
gat ggg gac acc acc atg agc ctg cat tct caa gcc tct gcc aca act Asp Gly Asp Thr Thr Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr 15 20 25 30 cgg cat cca gag ccc cgg cgc aca gtt ttt cag tac tac cag ctc tcc Arg His Pro Glu Pro Arg Arg Thr Val Phe Gln Tyr Tyr Gln Leu Ser	218

gga agt Gly Ser 80	ctg Leu	cag Gln	cat His	gtg Val	gct Ala 85	gaa Glu	aaa Lys	ctc Leu	tgt Cys	cgt Arg 90	gag Glu	ctg Leu	tat Tyr	aac Asn	410
aaa gct Lys Ala 95	gga Gly	ggc Gly	tat Tyr	aca Thr 100	aga Arg	aac Asn	atg Met	gtg Val	cca Pro 105	gca Ala	tct Ser	gct Ala	tct Ser	tct Ser 110	458
gag ago Glu Ser															506
agg tgo Arg Cys	agc Ser	cct Pro 130	tgt Cys	aca Thr	gaa Glu	caa Gln	tgg Trp 135	aaa Lys	tgg Trp	cat His	gga Gly	gac Asp 140	aat Asn	tgc Cys	554
tac cag Tyr Glr	ttc Phe 145	tat Tyr	aaa Lys	gac Asp	agc Ser	aaa Lys 150	agt Ser	tgg Trp	gag Glu	gac Asp	tgt Cys 155	aaa Lys	tat Tyr	ttc Phe	602
tgc ctt Cys Lei 160	ı Ser														650
ctg gaa Leu Gli 175															698
tgg aca Trp Th	a ggg	ctt Leu	ttg Leu 195	cgc Arg	cct Pro	gac Asp	agt Ser	ggc Gly 200	aag Lys	gcc Ala	tgg Trp	ctg Leu	tgg Trp 205	atg Met	746
gat gg: Asp Gl:	a acc / Thr	cct Pro 210	ttc Phe	act Thr	tct Ser	gaa Glu	ctg Leu 215	ttc Phe	cat His	att Ile	ata Ile	ata Ile 220	gat Asp	gtc Val	794
acc age Thr Se	c cca r Pro 225	aga Arg	agc Ser	aga Arg	gac Asp	tgt Cys 230	gtg Val	gcc Ala	atc Ile	ctt Leu	aat Asn 235	gly aaa	atg Met	atc Ile	842
ttc tc Phe Se 24	r Lys														890
gca gg Ala Gl [.] 255	a atg y Met	gtg Val	aag Lys	cca Pro 260	gag Glu	agc Ser	ctc Leu	cat His	gtc Val 265	ccc Pro	cct Pro	gaa Glu	aca Thr	tta Leu 270	938
ggc ga Gly Gl											ccta	ggt	tcta	gac	988

<210> 45

<211> 281

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature <223> n = a or c or g or t

<400> 45

Met Gln Ala Lys Tyr Ser Ser Thr Arg Asp Met Leu Asp Asp Asp Gly 1 10 15

Asp Thr Thr Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr Arg His 20 25 30

Pro Glu Pro Arg Arg Thr Val Phe Gln Tyr Tyr Gln Leu Ser Asn Thr 35 40 45

Gly Gln Asp Thr Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr Ser 50 60

Gln Glu Leu Gln Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly Ser 65 70 75 80

Leu Gln His Val Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys Ala 85 90 95

Gly Gly Tyr Thr Arg Asn Met Val Pro Ala Ser Ala Ser Ser Glu Ser 100 105 110

Leu Arg Gln Leu Pro His Met Gly Glu Ser Ala Ala Ala His Arg Cys
115 120 125

Ser Pro Cys Thr Glu Gln Trp Lys Trp His Gly Asp Asn Cys Tyr Gln 130 135 140

Phe Tyr Lys Asp Ser Lys Ser Trp Glu Asp Cys Lys Tyr Phe Cys Leu 145 150 155 160

Ser Glu Asn Ser Thr Met Leu Lys Ile Asn Lys Gln Glu Asp Leu Glu 165 170 175

Phe Ala Ala Ser Gln Ser Tyr Ser Glu Phe Phe Tyr Ser Tyr Trp Thr 180 185 190

Gly Leu Leu Arg Pro Asp Ser Gly Lys Ala Trp Leu Trp Met Asp Gly 195 200 205

Thr Pro Phe Thr Ser Glu Leu Phe His Ile Ile Ile Asp Val Thr Ser 210 215 220

Pro Arg Ser Arg Asp Cys Val Ala Ile Leu Asn Gly Met Ile Phe Ser 225 230 235 240

Lys Asp Cys Lys Glu Leu Lys Arg Cys Val Cys Glu Arg Arg Ala Gly
245 250 250

Met Val Lys Pro Glu Ser Leu His Val Pro Pro Glu Thr Leu Gly Glu 260 265 270

Gly Asp Met His His His His His His 275 280